

SEQUENCE LISTING

<110> Diversa Corporation

Kerovuo, Janne

Solbak, Arne

Gray, Kevin

McCann, Ryan

Purohit, Shalaka

Gerendash, Joel

Janssen, Giselle

Dahod, Samun

<120> PECTATE LYASES, NUCLEIC ACIDS ENCODING
THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462009640

<140> To Be Assigned

<141> Concurrently herewith

<150> 60/460,842

<151> 2003-04-04

<150> 60/484,798

<151> 2003-07-03

<160> 134

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1917

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 1

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acaattcaac	aagcgggtga	ccagggtccc	aaagacaata	cacacccggt	cttgattcag	180
atcaaaccgg	gtgtgtatca	ggaacagggt	cgtgtcgccg	ccggcaaacg	ctttatcact	240
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ggaaataccc	ggctggcatt	caccaccttc	gttaatgcag	acgactttcg	cgccgagaa	360
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gcagtcggaa	cgatcgcgtg	ggacgatgcy	cagaaaaaac	cgaacgagtg	gtatgcgagc	1020
gccgaggcgt	tgcgcattgc	cgacaacgtt	gttctttatc	aacgtgactc	cggcggttgg	1080
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gtgcgtaaga agaacgattc cacgatcgac aatggcgcgga cttacacgca actctcgttt 1200
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ccggcgagga cgtttgaatt agtttcgctg agtggtggtg aaagcgttga gatcgtgcg 1620
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<210> 2
 <211> 638
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (28)...(308)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (309)...(638)
 <223> Catalytic domain

<400> 2

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      20           25           30
Ala Asp Gly Ser Gly Asp Val Arg Thr Ile Gln Gln Ala Val Asp Gln
      35           40           45
Val Pro Lys Asp Asn Thr His Pro Val Leu Ile Gln Ile Lys Pro Gly
      50           55           60
Val Tyr Gln Glu Gln Val Arg Val Ala Ala Gly Lys Arg Phe Ile Thr
      65           70           75           80
Phe Arg Gly Asp Asp Ala Ser Lys Thr Val Ile Thr Tyr Arg Leu Ser
      85           90           95
Ala Leu Gln Ala Gly Asn Thr Arg Leu Ala Phe Thr Thr Phe Val Asn
      100          105          110
Ala Asp Asp Phe Arg Ala Glu Asn Leu Thr Phe Glu Asn Ser Phe Gly
      115          120          125
Thr Gly Ser Gln Ala Val Ala Leu Phe Val Asp Ala Asp Arg Ala Thr
      130          135          140
Phe Glu Asn Cys Arg Phe Leu Gly Trp Gln Asp Thr Leu Phe Val Asn
      145          150          155          160
Gly Ser Arg His Phe Phe Lys Asp Cys Tyr Val Glu Gly His Val Asp
      165          170          175
Phe Ile Phe Gly Thr Ala Ser Ala Val Phe Glu Asn Cys Thr Ile His
      180          185          190
Ser Lys Gly Glu Gly Tyr Val Thr Ala His Tyr Arg Thr Ser Asp Glu

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	195		200		205
Met	Asp Thr Gly Phe Val	Phe His Arg Cys Arg	Leu Thr Gly Arg Asp		
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Thr	Gly Arg Gly Val Tyr	Leu Gly Arg Pro Trp	Arg Pro Tyr Ala Arg		
225		230	235		240
Val	Val Phe Ile Asp Cys Trp	Leu Asp Ala His Ile	Arg Pro Glu Gly		
	245	250	255		
Trp	Asp Asn Trp Arg Asp	Pro Glu Arg Glu Lys	Thr Ala Trp Phe Ala		
	260	265	270		
Glu	Tyr Lys Ser Lys Gly	Pro Gly Ala Asn Pro	Val Ala Arg Val Ala		
	275	280	285		
Trp	Ser Arg Gln Leu Thr	Thr Glu Gln Ala Ala	Glu Phe Ser Arg Glu		
	290	295	300		
Arg	Phe Phe Ser Arg Ala	Val Arg Gly Leu Ser	Gly Gln Ala Asn Gln		
305		310	315		320
Ala	Val Gly Thr Ile Ala	Trp Asp Asp Ala	Gln Lys Lys Pro Asn	Glu	
	325	330	335		
Trp	Tyr Ala Ser Ala Glu	Ala Leu Arg Ile Ala	Asp Asn Val Val Leu		
	340	345	350		
Tyr	Gln Arg Asp Ser Gly	Gly Trp Pro Lys Asn	Ile Asp Met Gly Lys		
	355	360	365		
Pro	Leu Asp Glu Lys Gly	Arg Ala Gly Leu Leu	Arg Val Arg Lys Lys		
	370	375	380		
Asn	Asp Ser Thr Ile Asp	Asn Gly Ala Thr Tyr	Thr Gln Leu Ser Phe		
385		390	395		400
Leu	Ala Arg Val Tyr Thr	Ala Gln Lys Gln Glu	Arg His Arg Glu Ser		
	405	410	415		
Phe	Leu Lys Gly Leu Asp	Tyr Leu Leu Lys	Ala Gln Tyr Pro Asn	Gly	
	420	425	430		
Gly	Trp Pro Gln Phe Tyr	Pro Asn Leu Asn Gly	Tyr Tyr Lys His Ile		
	435	440	445		
Thr	Phe Asn Asp Asn Ala	Met Ile Gly Val Met	Lys Leu Leu Arg Asp		
	450	455	460		
Val	Ala Thr Ala Lys Pro	Ala Tyr Ala Phe Val	Asp Glu Ala Arg Arg		
465		470	475		480
Thr	Ser Ala Ala Lys Ala	Val Glu Lys Gly Ile	Glu Cys Ile Leu Lys		
	485	490	495		
Thr	Gln Val Val Val Asn	Gly Arg Arg Thr Val	Trp Cys Ala Gln His		
	500	505	510		
Asp	Glu Val Thr Leu Ala	Pro Ala Pro Ala Arg	Thr Phe Glu Leu Val		
	515	520	525		
Ser	Leu Ser Gly Gly Glu	Ser Val Glu Ile Val	Arg Phe Leu Met Ser		
	530	535	540		
Ile	Lys Asn Pro Ser Pro	Ala Val Val Glu Ala	Ile Glu Ser Ala Val		
545		550	555		560
Ala	Trp Phe Glu Gln Ser	Gln Val Lys Asp	Pro Ala Gly Lys Pro	Ala	
	565	570	575		
Trp	Ala Arg Phe Tyr Glu	Ile Gly Thr Asn Arg	Pro Ile Phe Ala Gly		
	580	585	590		
Arg	Asp Gly Val Val Lys	Tyr Asp Val Lys Gln	Ile Asp Glu Glu Arg		
	595	600	605		
Arg	Lys Asn Tyr Ala Trp	Tyr Val Asp Asp Ala	Ala Lys Leu Leu Lys		
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Thr	Asp Tyr Pro Glu Trp	Lys Glu Lys Asn Ala	Lys Asp Gln		
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<210> 3

<211> 1416

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 3

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atcgtgaaac	gcatcaagcg	acctcgtttc	ccgatgcgca	cgtttgatct	cacggagttt	180
ggagcgaaag	gtgatggacg	aacagattgc	acgttggttt	tccgtcgcgc	gatcgatcga	240
tgcacgaacg	ccggtgggtg	gagagtagtt	gttccaccgg	gttcgtatct	caactggcgc	300
attcatttga	agagcaacgt	cgaccttcat	atctcagaag	gtactacggt	caagttcagc	360
cagaaccgga	aagactacct	gcccgttggt	ttctcgcgtt	gggaaggcgt	cgagggtgtt	420
aactactcgc	cttttatcta	cgccttcgaa	caaacgaaca	ttgcgatcac	tggcaagggc	480
acgctcaacg	gtcaaagcga	caacgaacac	tggtggccct	ggaacggacg	tgccgcgtac	540
ggctggaaa	aagggatgag	caatcagcgt	cccgatcgaa	atgcgctggt	tgcgatggcc	600
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ttcattcaac	cttatcggtg	tgagaacgtg	ctgatcgaag	gtgtcactat	tcgaaactcg	720
ccgatgtggg	aaattcatcc	ggtgctctgc	cggaatgtca	tcgtccaaaa	tgtgatcatc	780
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gatggtcacg	gcgggattac	ggtgggcagc	gagatttcgg	gtgggggtgcg	aaatcttttc	1020
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ccagtcgttc	gtgattacac	cgtcgatggc	cttcgcagca	cgaaaagtaa	gtacgcgctc	1260
gatgtgcagg	gcttggcgac	ggcgccgatc	gtgaatctgc	gtctaaccac	ctgcatcttc	1320
gacaatgtcg	ctgaaggaaa	tgttgtagaag	aacgtaaagg	atgcaactat	cgagaatgtc	1380
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<210> 4

<211> 471

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(28)

<221> DOMAIN

<222> (81)...(476)

<223> Catalytic domain

<400> 4

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		20					25						30		
Pro	Trp	Glu	Thr	Val	Met	Pro	Ser	Ile	Val	Lys	Arg	Ile	Lys	Arg	Pro
		35				40					45				
Arg	Phe	Pro	Met	Arg	Thr	Phe	Asp	Leu	Thr	Glu	Phe	Gly	Ala	Lys	Gly
	50				55					60					
Asp	Gly	Arg	Thr	Asp	Cys	Thr	Leu	Ala	Phe	Arg	Arg	Ala	Ile	Asp	Arg
65					70				75					80	
Cys	Thr	Asn	Ala	Gly	Gly	Gly	Arg	Val	Val	Pro	Pro	Gly	Ser	Tyr	
			85					90						95	

Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asp	Leu	His	Ile	Ser
			100					105					110		
Glu	Gly	Thr	Thr	Val	Lys	Phe	Ser	Gln	Asn	Pro	Lys	Asp	Tyr	Leu	Pro
			115				120					125			
Val	Val	Phe	Ser	Arg	Trp	Glu	Gly	Val	Glu	Val	Phe	Asn	Tyr	Ser	Pro
			130			135					140				
Phe	Ile	Tyr	Ala	Phe	Glu	Gln	Thr	Asn	Ile	Ala	Ile	Thr	Gly	Lys	Gly
145					150					155					160
Thr	Leu	Asn	Gly	Gln	Ser	Asp	Asn	Glu	His	Trp	Trp	Pro	Trp	Asn	Gly
				165					170					175	
Arg	Ala	Ala	Tyr	Gly	Trp	Lys	Glu	Gly	Met	Ser	Asn	Gln	Arg	Pro	Asp
			180					185					190		
Arg	Asn	Ala	Leu	Phe	Ala	Met	Ala	Glu	Lys	Gly	Val	Pro	Val	Gln	Glu
			195				200					205			
Arg	Ile	Phe	Gly	Glu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro
			210			215					220				
Tyr	Arg	Cys	Glu	Asn	Val	Leu	Ile	Glu	Gly	Val	Thr	Ile	Arg	Asn	Ser
225				230						235					240
Pro	Met	Trp	Glu	Ile	His	Pro	Val	Leu	Cys	Arg	Asn	Val	Ile	Val	Gln
				245					250					255	
Asn	Val	Ile	Ile	Asn	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asn	Pro
			260					265					270		
Glu	Ser	Cys	Thr	Asp	Val	Leu	Ile	Lys	Asp	Cys	Asp	Phe	Asp	Thr	Gly
			275				280					285			
Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ser	Gly	Arg	Asn	Ala	Asp	Gly	Arg	Arg
			290			295					300				
Leu	Lys	Ala	Pro	Thr	Glu	Asn	Ile	Ile	Val	Thr	Gly	Cys	Arg	Met	Lys
305					310					315					320
Asp	Gly	His	Gly	Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val
				325					330					335	
Arg	Asn	Leu	Phe	Ala	Ser	Asn	Cys	Arg	Leu	Asp	Ser	Pro	Asn	Leu	Asp
			340					345					350		
His	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Met	Arg	Gly	Gly	Leu	Leu	Glu
			355				360					365			
Asn	Leu	His	Phe	Arg	Asn	Ile	Asp	Val	Gly	Gln	Val	Ala	His	Ala	Val
			370			375					380				
Ile	Thr	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Phe	Thr
385				390						395					400
Pro	Val	Val	Arg	Asp	Tyr	Thr	Val	Asp	Gly	Leu	Arg	Ser	Thr	Lys	Ser
				405					410					415	
Lys	Tyr	Ala	Leu	Asp	Val	Gln	Gly	Leu	Ala	Thr	Ala	Pro	Ile	Val	Asn
			420				425					430			
Leu	Arg	Leu	Thr	Asn	Cys	Ile	Phe	Asp	Asn	Val	Ala	Glu	Gly	Asn	Val
			435				440					445			
Val	Lys	Asn	Val	Lys	Asp	Ala	Thr	Ile	Glu	Asn	Val	Lys	Ile	Asn	Gly
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Lys	Ser	Val	Asp	Ala	Val	Pro									
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<210> 5

<211> 1077

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

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60

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gacaacggcg cgacgacaac ccagctcgcg tatctggcga aggtcatcac ggccaagaat 300
atcgaaagcc atcgcgtcgc gtttttcaaa ggccctcgatt ttcttttcgc catgcagtac 360
gggaatggcg gcttcccgcga attttttcct ctgctgacg attattcgcg cgagattacg 420
ttcaacgaca acgcgatgat aaatgtgctt cggttgctcc gcgacatagc cgatcgaag 480
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gcgcagtatg atgagaagac attgaagccg gccgcggcgc gaaagtctga gccggcatca 660
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<210> 6
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(358)
 <223> Catalytic domain

<400> 6

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		20						25					30		
Glu	Ala	Thr	Arg	Ile	Ala	Asn	Gln	Val	Ile	Leu	Tyr	Gln	Arg	Asp	Asn
		35					40					45			
Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Ala	Ala	Met	Leu	Met	Gln	Ala
	50					55					60				
Glu	Arg	Glu	Lys	Leu	Ser	Arg	Glu	Lys	Ser	Glu	Thr	Asp	Thr	Thr	Ile
65					70					75				80	
Asp	Asn	Gly	Ala	Thr	Thr	Thr	Gln	Leu	Ala	Tyr	Leu	Ala	Lys	Val	Ile
			85						90					95	
Thr	Ala	Lys	Asn	Ile	Glu	Ser	His	Arg	Val	Ala	Phe	Phe	Lys	Gly	Leu
		100						105					110		
Asp	Phe	Leu	Phe	Ala	Met	Gln	Tyr	Gly	Asn	Gly	Gly	Phe	Pro	Gln	Phe
		115					120					125			
Phe	Pro	Leu	Arg	Asp	Asp	Tyr	Ser	Arg	Glu	Ile	Thr	Phe	Asn	Asp	Asn
	130					135					140				
Ala	Met	Ile	Asn	Val	Leu	Arg	Leu	Leu	Arg	Asp	Ile	Ala	Asp	Arg	Lys
145					150					155					160
Asn	Asp	Tyr	Val	Phe	Val	Asp	Glu	Glu	Arg	Ala	Lys	Ala	Glu	Gln	
			165						170					175	
Ala	Val	Arg	Arg	Ala	Ile	Pro	Leu	Ile	Leu	Ser	Thr	Gln	Val	Val	Val
		180						185					190		
Asp	Gly	Lys	Lys	Thr	Val	Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Lys	Thr	Leu
		195					200					205			
Lys	Pro	Ala	Ala	Ala	Arg	Lys	Phe	Glu	Pro	Ala	Ser	Leu	Thr	Ala	Gly
	210					215					220				

Glu	Ser	Val	Gly	Ile	Val	Arg	Phe	Leu	Met	Leu	Glu	Lys	Pro	Thr	Pro
225					230					235					240
Glu	Ile	Ile	Asn	Ala	Ile	Glu	Ser	Ala	Ile	Ala	Trp	Tyr	Lys	Ala	Asn
			245						250					255	
Asn	Ile	Ser	Gly	Leu	Arg	Trp	Glu	Arg	Arg	Asn	Gly	Glu	Asn	Ile	Val
			260					265					270		
Ile	Lys	Asp	Lys	Asn	Ala	Pro	Pro	Val	Trp	Ala	Arg	Phe	Tyr	Gln	Ile
		275					280					285			
Glu	Thr	Met	Arg	Pro	Ile	Phe	Ala	Gly	Arg	Asp	Ala	Val	Ile	Arg	Tyr
	290					295					300				
Asp	Val	Met	Gln	Ile	Glu	Ser	Glu	Arg	Arg	Asn	Gly	Tyr	Ala	Trp	Tyr
305				310						315					320
Val	Ser	Glu	Pro	Asn	Glu	Leu	Leu	Asn	Glu	Asp	Tyr	Pro	Lys	Trp	Arg
			325					330						335	
Thr	Arg	Ser	Ala	Lys	Arg	Ala	Gln	Ile	Phe	Gln	Arg	Pro	Pro	Leu	Gly
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Ser	Arg	Phe	Arg	Thr	Val										
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<210> 7
 <211> 1125
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 7

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ccggcggcga	tccgtgggg	agcggacgtc	ctgcggcaga	agccggagtg	gtatgcctcg		180	
cgagaggcga	ggacgatcgc	cgacagcgtc	atccagtacc	aggcggcgga	cgggcggtgg		240	
cccaagaaca	ccgacctcg	gactccgcc	acggctgaat	cacgcgcgg	cgcgcgcc		300	
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ctggtggcg	acgcgaccg	cgaggctcgc	tatcgcggt	cgttcctccg	cggttcgac		420	
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gggtattaca	cccacatcac	cttcaacgac	aacgcgatgg	tcaacgtgct	gaccgtgctg		540	
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gcccgcgccg	ccgtgtccc	ggggatcgac	gtcatcctga	agaccaagt	gaaacagaac		660	
ggcaagctga	cgcgctggg	cgcgacgac	gacgagaaga	ccctcgccg	ggcggtggcg		720	
cgcgcttacg	agccgccatc	gctctccggc	agcgaaaccg	tcggcatcgt	ccgttcctg		780	
atggagatcg	agaagccgtc	accggagatc	gtcgccgcga	tcgaaggggc	cgtcgcctgg		840	
ctgaagtccg	tggcgattcc	ggggctgcgc	tacgagtcct	tcaccggcgc	ggacggacag		900	
agggaccgcc	gcgtcggtcc	ggatccatcg	gccggactcc	tgtgggcgcg	gttctacgag		960	
ctcggcacca	accggccgat	cttcctcggc	cgcgactccg	tggttcggc	cgcgctcagt		1020	
gacatcgaac	gcgagcgccg	cgccggctac	gcctactacg	gtacgtggcc	ggcgagcctg		1080	
attgctgcgg	actaccgcg	ctggcgttcg	acgctccggc	gctga			1125	

<210> 8
 <211> 374
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(374)
 <223> Catalytic domain

<400> 8

Met His Ala Gly Ala Lys His Val Ser Arg Trp Arg Glu Glu Phe Leu
 1 5 10 15
 Arg Asp Phe Ala Ala Arg Leu Ser Arg Thr Ile Pro Ser Ser Pro Ala
 20 25 30
 Gln Ser Ala Ala Val Ser Gly Val Pro Ala Ala Ile Arg Trp Gly Ala
 35 40 45
 Asp Val Leu Arg Gln Lys Pro Glu Trp Tyr Ala Ser Arg Glu Ala Arg
 50 55 60
 Thr Ile Ala Asp Ser Val Ile Gln Tyr Gln Ala Ala Asp Gly Gly Trp
 65 70 75 80
 Pro Lys Asn Thr Asp Leu Gly Thr Pro Pro Thr Ala Glu Ser Arg Ala
 85 90 95
 Gly Ala Ala Ala Asp Val Thr Ser Ser Thr Ile Asp Asn Asn Gly Thr
 100 105 110
 Thr Met Pro Met Gln Phe Leu Ala Leu Val Ala Asp Ala Thr Gly Glu
 115 120 125
 Ala Arg Tyr Arg Ala Ser Phe Leu Arg Gly Phe Asp Tyr Leu Leu Ala
 130 135 140
 Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Phe Phe Pro Leu Arg Arg
 145 150 155 160
 Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asn Ala Met Val Asn Val
 165 170 175
 Leu Thr Val Leu Arg Asp Ala Ala Ala Gly Gln Ala Pro Tyr Ala Phe
 180 185 190
 Val Asp Glu Pro Arg Arg Ala Lys Ala Arg Ala Ala Val Ser Arg Gly
 195 200 205
 Ile Asp Val Ile Leu Lys Thr Gln Val Lys Gln Asn Gly Lys Leu Thr
 210 215 220
 Ala Trp Cys Ala Gln His Asp Glu Lys Thr Leu Ala Pro Ala Trp Ala
 225 230 235 240
 Arg Ala Tyr Glu Pro Pro Ser Leu Ser Gly Ser Glu Thr Val Gly Ile
 245 250 255
 Val Arg Phe Leu Met Glu Ile Glu Lys Pro Ser Pro Glu Ile Val Ala
 260 265 270
 Ala Ile Glu Gly Ala Val Ala Trp Leu Lys Ser Val Ala Ile Pro Gly
 275 280 285
 Leu Arg Tyr Glu Ser Phe Thr Gly Ala Asp Gly Gln Arg Asp Arg Arg
 290 295 300
 Val Val Pro Asp Pro Ser Ala Gly Leu Leu Trp Ala Arg Phe Tyr Glu
 305 310 315 320
 Leu Gly Thr Asn Arg Pro Ile Phe Leu Gly Arg Asp Ser Val Val Arg
 325 330 335
 Ala Ala Leu Ser Asp Ile Glu Arg Glu Arg Arg Ala Gly Tyr Ala Tyr
 340 345 350
 Tyr Gly Thr Trp Pro Ala Ser Leu Ile Ala Ala Asp Tyr Pro Arg Trp
 355 360 365
 Arg Ser Thr Leu Arg Arg
 370

<210> 9

<211> 1116

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

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<400> 9
ttgatcggtgta gcatgaaaac gattctctca aatctgaacg cggcgctgct ttcatgcgcc      60
ctgctctttg cggcagccac acaggaacc aagccgccg aagtgcggtg gaatgagtg      120
ctaaaccaa aacctgcctg gtacggcagc ccggaagcgg tgcgcattgc tgacaacctg      180
ttgctttacc aacgcgacca cggcggtggt cacaagaata tcgaaatggc tgcggtcttg      240
accgaacagc aacaggcaga gttgaaagcg caaaaggcaa ccgacgattc gacgattgat      300
aacggcgcgga cctataccca ggtgatttat ctggcgcgcg tcttcaatgc gacgaagcag      360
gagcgattca aaaccgcgtt tctcaaagga ttcgattatc tgctcaaggc tcagtatgcg      420
aacggcggtt ggccgcagta ttaccgcgtt ttgcagggtt attacaaaca catcacgttc      480
aacgatgacg cgatggtcgg cgtgcttgat cttctgcgcg atgttgcgcg cggcgattcc      540
ggttatcggt tcgtggacag cgaccggcgc gcccgcgcca gccaggccgt gcaaaaagga      600
attgagtgca tcttgaaatg ccagatcgtg gtccgcggga aaaagaccgc ctggtgcgcg      660
caacacgatg aagtgcatt cgccccgcg ccggcacgca cctacgagaa aatttcgctg      720
agcggcagcg aatcggttg cctgatccgc ttctgatgg gcattgaaca accggacgcg      780
cgtgtagttg aggcgattga gtccgcggtt gcctggctca agcaagccaa gctgaccgac      840
atcaaagtgg ttcagaaggc ggatgcttcg aagcccaatg gcttcgaccg ggtcgtcgtt      900
gaagatgcac aagccgggcc attgtgggcg cgcttttacg agatcggtac gggccgcccg      960
atcttttccg gacgtgacgg catcgtcaaa tacagcttgg cggaaatcga acacgaacgg     1020
cgcacgggct acggctggta cacgaatgcg cccgcgaaat tgctggaaca agattatccg     1080
gcctggcaaa tcaaacgcgg gggcaagaaa aagtaa                                1116

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<210> 10
<211> 371
<212> PRT
<213> Unknown

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<220>
<223> Obtained from an environmental sample

```

```

<221> SIGNAL
<222> (1)...(29)

```

```

<221> DOMAIN
<222> (30)...(371)
<223> Catalytic domain

```

```

<400> 10
Met Ile Gly Ser Met Lys Thr Ile Leu Ser Asn Leu Asn Ala Ala Leu
 1           5           10           15
Leu Ser Cys Ala Leu Leu Phe Ala Ala Ala Thr Gln Gly Thr Lys Pro
 20           25           30
Pro Glu Val Arg Trp Asn Glu Cys Leu Asn Gln Lys Pro Ala Trp Tyr
 35           40           45
Gly Ser Pro Glu Ala Val Arg Ile Ala Asp Asn Leu Leu Leu Tyr Gln
 50           55           60
Arg Asp His Gly Gly Trp His Lys Asn Ile Glu Met Ala Ala Val Leu
 65           70           75           80
Thr Glu Gln Gln Gln Ala Glu Leu Lys Ala Gln Lys Ala Thr Asp Asp
 85           90           95
Ser Thr Ile Asp Asn Gly Ala Thr Tyr Thr Gln Val Ile Tyr Leu Ala
 100          105          110
Arg Val Phe Asn Ala Thr Lys Gln Glu Arg Phe Lys Thr Ala Phe Leu
 115          120          125
Lys Gly Phe Asp Tyr Leu Leu Lys Ala Gln Tyr Ala Asn Gly Gly Trp
 130          135          140
Pro Gln Tyr Tyr Pro Arg Leu Gln Gly Tyr Tyr Lys His Ile Thr Phe
 145          150          155          160
Asn Asp Asp Ala Met Val Gly Val Leu Asp Leu Leu Arg Asp Val Ala
 165          170          175

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Arg Gly Asp Ser Gly Tyr Arg Phe Val Asp Ser Asp Arg Arg Ala Arg
 180 185 190
 Ala Ser Gln Ala Val Gln Lys Gly Ile Glu Cys Ile Leu Lys Cys Gln
 195 200 205
 Ile Val Val Ala Gly Lys Lys Thr Ala Trp Cys Ala Gln His Asp Glu
 210 215 220
 Val Thr Phe Ala Pro Ala Pro Ala Arg Thr Tyr Glu Lys Ile Ser Leu
 225 230 235 240
 Ser Gly Ser Glu Ser Val Gly Leu Ile Arg Phe Leu Met Gly Ile Glu
 245 250 255
 Gln Pro Asp Ala Arg Val Val Glu Ala Ile Glu Ser Ala Val Ala Trp
 260 265 270
 Leu Lys Gln Ala Lys Leu Thr Gly Ile Lys Val Val Gln Lys Ala Asp
 275 280 285
 Ala Ser Lys Pro Asn Gly Phe Asp Arg Val Val Val Glu Asp Ala Gln
 290 295 300
 Ala Gly Pro Leu Trp Ala Arg Phe Tyr Glu Ile Gly Thr Gly Arg Pro
 305 310 315 320
 Ile Phe Ser Gly Arg Asp Gly Ile Val Lys Tyr Ser Leu Ala Glu Ile
 325 330 335
 Glu His Glu Arg Arg Thr Gly Tyr Gly Trp Tyr Thr Asn Ala Pro Ala
 340 345 350
 Lys Leu Leu Glu Gln Asp Tyr Pro Ala Trp Gln Ile Lys Arg Gly Gly
 355 360 365
 Lys Lys Lys
 370

<210> 11
 <211> 1167
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 11
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 ggtggttgagg caaagttggt cgatcgcgag cggttcttca gcctcgctgc ggaacgaacc 120
 tctaagaaga atgaccagca agtcggcgcc atcgcggtgga aagatgcaca cggaaaggca 180
 gatgagtggg atgagagcgt tgaggcactt cgtatagccg ataacgtcgt tttctatcaa 240
 cgtgactcag gtggctggcc caagaatata gagatggcga agacgttgag cgatcgtag 300
 aaggctgcga ttctccgcga gaagaaaaag aatgactcaa caatcgacaa tggcgcgact 360
 cacactcagt tatcttttct ggcgcgcgct tatacagcac aacagcagga gcgacatcg 420
 gagtcatttt taaaaggact ggattactta ctgaaggcgc agtattcaaa tggtggttg 480
 ccacagttct atccaaactt gaatggctac tacaacgga tcacgtacaa cgatggcgcg 540
 atgatcggtg tgatgaagct tctgcgtgat gttgcggcag cgaaacctga atacgcgttt 600
 gtcgatgaaa ctcggcgtgc gaaggctgcg aacgcggttg aaaaaggcat cgtgtgcatt 660
 ttgaaaacgc aggtgggttg tgatgggcgt cgcactgttt ggtgtgcaca acacgacgaa 720
 gtgacgtttg cgcccgcgcc tgcaagaaag tttgagttag cttcgttgag cggcggtag 780
 agcgctcgata ttgttcgatt tctaattgtc ataaaggatc catcgcgtaa cgtggttgaa 840
 tcgattgaat cggcagttaa atggtttgag cagtcggagc taaaaggcgt taagtgggtc 900
 aagaaaaccg acgctactca acctaattggg ttcgattgtg tcgttggtta agatccggag 960
 agctctgttt gggcgcgctt ttacgagatt ggcacgaacc gcccgatctt tgccgggctg 1020
 gatggagtgc ctaagtatga cgtcgcgcag atcgaacacg agcgacgaac gggttacgaa 1080
 tggtagcttg atgaggcagc aaaactgctg aaaaaagatt atccggcgtg gaagaaacga 1140
 catgtcgtca cgacgcgagt tcattag 1167

<210> 12
 <211> 388

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(388)

<223> Catalytic domain

<400> 12

Met	Ser	Leu	Gly	Pro	Gly	Ala	Asn	Pro	Lys	Ala	Arg	Val	Pro	Trp	Ser
1				5					10					15	
Lys	Gln	Leu	Ser	Gly	Val	Glu	Ala	Lys	Leu	Phe	Asp	Arg	Glu	Arg	Phe
		20						25					30		
Phe	Ser	Leu	Ala	Ala	Glu	Arg	Thr	Ser	Lys	Lys	Asn	Asp	Gln	Gln	Val
		35					40					45			
Gly	Ala	Ile	Ala	Trp	Lys	Asp	Ala	His	Gly	Lys	Ala	Asp	Glu	Trp	Tyr
		50				55					60				
Ala	Ser	Val	Glu	Ala	Leu	Arg	Ile	Ala	Asp	Asn	Val	Val	Phe	Tyr	Gln
65					70					75					80
Arg	Asp	Ser	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Glu	Met	Ala	Lys	Thr	Leu
				85					90					95	
Ser	Asp	Arg	Glu	Lys	Ala	Ala	Ile	Leu	Arg	Glu	Lys	Lys	Lys	Asn	Asp
			100					105					110		
Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	His	Thr	Gln	Leu	Ser	Phe	Leu	Ala
		115					120					125			
Arg	Val	Tyr	Thr	Ala	Gln	Gln	Glu	Arg	His	Arg	Glu	Ser	Phe	Leu	
		130				135				140					
Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Lys	Ala	Gln	Tyr	Ser	Asn	Gly	Gly	Trp
145					150					155					160
Pro	Gln	Phe	Tyr	Pro	Asn	Leu	Asn	Gly	Tyr	Tyr	Lys	Arg	Ile	Thr	Tyr
				165				170						175	
Asn	Asp	Gly	Ala	Met	Ile	Gly	Val	Met	Lys	Leu	Leu	Arg	Asp	Val	Ala
			180					185					190		
Ala	Ala	Lys	Pro	Glu	Tyr	Ala	Phe	Val	Asp	Glu	Thr	Arg	Arg	Ala	Lys
		195					200					205			
Ala	Ala	Asn	Ala	Val	Glu	Lys	Gly	Ile	Val	Cys	Ile	Leu	Lys	Thr	Gln
		210				215					220				
Val	Val	Val	Asp	Gly	Arg	Arg	Thr	Val	Trp	Cys	Ala	Gln	His	Asp	Glu
225				230						235					240
Val	Thr	Phe	Ala	Pro	Ala	Pro	Ala	Arg	Lys	Phe	Glu	Leu	Ala	Ser	Leu
				245					250					255	
Ser	Gly	Gly	Glu	Ser	Val	Asp	Ile	Val	Arg	Phe	Leu	Met	Ser	Ile	Lys
			260					265					270		
Asp	Pro	Ser	Arg	Asn	Val	Val	Glu	Ser	Ile	Glu	Ser	Ala	Val	Lys	Trp
		275					280					285			
Phe	Glu	Gln	Ser	Glu	Leu	Lys	Gly	Val	Lys	Trp	Val	Lys	Lys	Thr	Asp
	290					295					300				
Ala	Thr	Gln	Pro	Asn	Gly	Phe	Asp	Cys	Val	Val	Val	Lys	Asp	Pro	Glu
305					310					315					320
Ser	Ser	Val	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile
				325					330					335	
Phe	Ala	Gly	Arg	Asp	Gly	Val	Pro	Lys	Tyr	Asp	Val	Ala	Gln	Ile	Glu
		340						345					350		
His	Glu	Arg	Arg	Thr	Gly	Tyr	Glu	Trp	Tyr	Val	Asp	Glu	Ala	Ala	Lys
		355					360					365			
Leu	Leu	Lys	Lys	Asp	Tyr	Pro	Ala	Trp	Lys	Lys	Arg	His	Val	Val	Thr
	370					375					380				

Thr Arg Val His
385

<210> 13
<211> 1065
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 13
atgaaaacga tcagccttat ttgcctcgca atctctgctg ggattctgga ttcggttgcg 60
gcggcacgct ggaacgaatt cgcccagaag gcggatgatt ggtatcgagg tgacgaaggc 120
aggcgcggtt cttcgaatat tctttctcac caatcactgc aaggaagctg gcccaagaat 180
accgatacca ccgcgagatt cttcaatgga gatctagcga agattcaggg cacgttcgac 240
aacggtgcga cgacggacga gttgcgtttc ctggcccgcg cgtttgtcgc cacgaaagaa 300
aaaaactacg agtcagcggt ccgaaaaggc ttcgaacaca ttctcgcggc gcaatacgcg 360
aacggcggat ggccgcaata ttccgcccgc cccaaaagtt accaccgaca cattaccttc 420
aacgataaatt cgatggtgcg gctgatgatt ttcttctcgc aggtcacgac ttcgaatctc 480
tactcggttcg tcgaagcgcc gctgcgaaca caagcccgcg aaagtttcga tcgcggtgtg 540
cgggtgcattc ttaagtgccg gatcgctcgtg aacgggcaca agaccgcgtg gtgcgcgcaa 600
catgatgaaa cggatttcag ccccgatcc gcgcgtagtt acgaactgcc ttcgctgagc 660
ggttctgaat cagtcggcat tgtgcgcttg ctgatgagcc tcgatcagcc gagccgcgga 720
gtgatcgatg ccatacacia cgcgtagcgt tggttcgaat cggcgaagct gcccgggatc 780
aaaaccgttc aagagaccga tccgaattcg cccaaaaggct ggaatcgcgt cgtcgtaaaa 840
gatgaaagtg cccgaccgat gtgggcgcgt ttctacgaca tcaacaccaa caaaccgttc 900
ttttgtgatc gcgatggtgt gccaaagccg agtcttgccg agatcgggta tgaacggcgg 960
aacggttatg cgtggctcgg atactggcct gaagacttgc tcgcaagaga gtatccagcg 1020
tggaagatga agtggctgaa gcccaaagag cgcccagcat tttga 1065

<210> 14
<211> 354
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<221> DOMAIN
<222> (23)...(354)
<223> Catalytic domain

<400> 14
Met Lys Thr Ile Ser Leu Ile Cys Leu Ala Ile Ser Ala Gly Ile Leu
1 5 10 15
Asp Ser Val Ala Ala Arg Trp Asn Glu Phe Ala Gln Lys Ala Asp
20 25 30
Asp Trp Tyr Arg Gly Asp Glu Gly Arg Arg Val Ala Ser Asn Ile Leu
35 40 45
Ser His Gln Ser Leu Gln Gly Ser Trp Pro Lys Asn Thr Asp Thr Thr
50 55 60
Ala Arg Phe Phe Asn Gly Asp Leu Ala Lys Ile Gln Gly Thr Phe Asp
65 70 75 80
Asn Gly Ala Thr Thr Asp Glu Leu Arg Phe Leu Ala Arg Ala Phe Val
85 90 95

Ala Thr Lys Glu Lys Asn Tyr Glu Ser Ala Phe Arg Lys Gly Phe Glu
 100 105 110
 His Ile Leu Ala Ala Gln Tyr Ala Asn Gly Gly Trp Pro Gln Tyr Ser
 115 120 125
 Pro Pro Pro Lys Ser Tyr His Arg His Ile Thr Phe Asn Asp Asn Ser
 130 135 140
 Met Val Arg Leu Met Ile Phe Leu Arg Glu Val Thr Thr Ser Asn Leu
 145 150 155 160
 Tyr Ser Phe Val Glu Ala Pro Leu Arg Thr Gln Ala Arg Glu Ser Phe
 165 170 175
 Asp Arg Gly Val Arg Cys Ile Leu Lys Cys Gln Ile Val Val Asn Gly
 180 185 190
 His Lys Thr Ala Trp Cys Ala Gln His Asp Glu Thr Asp Phe Ser Pro
 195 200 205
 Arg Ser Ala Arg Ser Tyr Glu Leu Pro Ser Leu Ser Gly Ser Glu Ser
 210 215 220
 Val Gly Ile Val Arg Leu Leu Met Ser Leu Asp Gln Pro Ser Arg Gly
 225 230 235 240
 Val Ile Asp Ala Ile Thr Asn Ala Val Ala Trp Phe Glu Ser Ala Lys
 245 250 255
 Leu Pro Gly Ile Lys Thr Val Gln Glu Thr Asp Pro Asn Ser Pro Lys
 260 265 270
 Gly Trp Asn Arg Val Val Val Lys Asp Glu Ser Ala Arg Pro Met Trp
 275 280 285
 Ala Arg Phe Tyr Asp Ile Asn Thr Asn Lys Pro Phe Phe Cys Asp Arg
 290 295 300
 Asp Gly Val Pro Lys Pro Ser Leu Ala Glu Ile Gly Tyr Glu Arg Arg
 305 310 315 320
 Asn Gly Tyr Ala Trp Leu Gly Tyr Trp Pro Glu Asp Leu Leu Ala Arg
 325 330 335
 Glu Tyr Pro Ala Trp Lys Met Lys Trp Leu Lys Pro Lys Glu Arg Pro
 340 345 350
 Ala Phe

<210> 15
 <211> 1575
 <212> DNA
 <213> Bacteria

<400> 15
 atgagacgac cagtcgcact ccggctccac gcggcactgg ccaccctggc cctggcggcc 60
 gcgaccggcg tgggtgctctc gatccccag gcatcgggcg cgcccgggcg cgccaccggc 120
 tacgccggcc agaacggcg caccaccggc ggtgccggcg gccagaccgt acggggccacc 180
 acggggcaccg ccatccacgc ggccctgtgc ggacgggcca gcagcagcac cccgatcacg 240
 atcgaggtcg agggaacgat caaccacgcc aacaccgcca aggtgtccgg cccagctgc 300
 aacaccgccc ccggagtgat cgagctgaag cagatcagca acgtcacgct cgtcggggtc 360
 ggctccggcg ccgtcttcga ccaactcggc atccacatcc gcgagtcag caacatcatc 420
 atccagaacg tgacggtccg gaacgtcaag aagtcgggct cgccgctgtc caacggcggc 480
 gacgccatcg gcatggagag cgacgtccgc aacgtctggg tcgaccactc caccctggag 540
 gcctcggggcg gcgagtcgga gggctacgac ggcctcttcg acatgaagga caacaccgg 600
 tacgtgaccc tgtcgtacag catcctgcgc aaatccgggc gcggcgccct cgtgggggtcc 660
 agcgagaccg aactctcgaa cagcttcac acgtaccacc acaacctgta cgagaacatc 720
 gactcgcgcg cgccctgct gcgcggcggg accgcccaca tgtacaacaa ccactacctg 780
 cggatcaacg agtccggcat caactcccgt gccggagccc acgccaaggt ggacaacaac 840
 tacttcgagg actccaagga cgtcctcggc acctcttaca ccgacgccc cgggtactgg 900
 caggtcagcg gcaacgtcta cgacaacgtg acctgggtccg cccggggcac cgacaacaac 960
 ccggcggggc cggaccgcga gtccaacacc accgtctcca tcccctacgc cttcagcctc 1020
 gaccgggcca cctgcgtgcc ggacgtcgtg agccgaacgg cgggtgccgg caagggactt 1080

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cagggtgtcga acggcagctg ctccccgcag acacccacgc ccacgccgac gggcacgccg 1140
accacacccg cgccgacgac tcccaccccg agcccgacgc cctccacgcc cggaccgacc 1200
cagcccggcg ggacgaacct cagcatcggt gccgggtccg acggttcgag caaggccgac 1260
ggcaccagct acggcaacgt ccgggacggg gacctcggca cccactggtc tccggccggt 1320
tcgaccggct ccgtgtcgat caagtggggc agcgccacca cggctctccg catcgtcatc 1380
cgcgaggcgg cgggcgcgac gggcgtcatc ggctcctggc tcgtcctgaa cggcgacacc 1440
ggcgccgtgc tgacctccg cagcggggcg gggacgatct ccgtccccg gacggccctg 1500
aagaagatca ccttcgagat cacgggcgcg agcggcacgc cacggatcgc cgagttcgag 1560
acgtacgccg gctag 1575

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```

<210> 16
<211> 524
<212> PRT
<213> Bacteria

```

```
<220>
```

```

<221> SIGNAL
<222> (1)...(33)

```

```

<221> DOMAIN
<222> (34)...(359)
<223> Catalytic domain

```

```
<400> 16
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```

Met Arg Arg Pro Val Ala Leu Arg Leu His Ala Ala Leu Ala Thr Leu
 1          5          10          15
Ala Leu Ala Ala Thr Gly Val Val Leu Ser Ile Pro Gln Ala Ser
 20          25          30
Ala Ala Ala Gly Gly Ala Thr Gly Tyr Ala Gly Gln Asn Gly Gly Thr
 35          40          45
Thr Gly Gly Ala Gly Gly Gln Thr Val Arg Ala Thr Thr Gly Thr Ala
 50          55          60
Ile His Ala Ala Leu Cys Gly Arg Ala Ser Ser Thr Pro Ile Thr
 65          70          75          80
Ile Glu Val Glu Gly Thr Ile Asn His Ala Asn Thr Ala Lys Val Ser
 85          90          95
Gly Pro Ser Cys Asn Thr Ala Ala Gly Val Ile Glu Leu Lys Gln Ile
100          105          110
Ser Asn Val Thr Leu Val Gly Val Gly Ser Gly Ala Val Phe Asp Gln
115          120          125
Leu Gly Ile His Ile Arg Glu Ser Ser Asn Ile Ile Ile Gln Asn Val
130          135          140
Thr Val Arg Asn Val Lys Lys Ser Gly Ser Pro Leu Ser Asn Gly Gly
145          150          155          160
Asp Ala Ile Gly Met Glu Ser Asp Val Arg Asn Val Trp Val Asp His
165          170          175
Ser Thr Leu Glu Ala Ser Gly Gly Glu Ser Glu Gly Tyr Asp Gly Leu
180          185          190
Phe Asp Met Lys Asp Asn Thr Arg Tyr Val Thr Leu Ser Tyr Ser Ile
195          200          205
Leu Arg Lys Ser Gly Arg Gly Gly Leu Val Gly Ser Ser Glu Thr Glu
210          215          220
Leu Ser Asn Ser Phe Ile Thr Tyr His His Asn Leu Tyr Glu Asn Ile
225          230          235          240
Asp Ser Arg Ala Pro Leu Leu Arg Gly Gly Thr Ala His Met Tyr Asn
245          250          255
Asn His Tyr Leu Arg Ile Asn Glu Ser Gly Ile Asn Ser Arg Ala Gly
260          265          270

```

Ala His Ala Lys Val Asp Asn Asn Tyr Phe Glu Asp Ser Lys Asp Val
 275 280 285
 Leu Gly Thr Phe Tyr Thr Asp Ala Ala Gly Tyr Trp Gln Val Ser Gly
 290 295 300
 Asn Val Tyr Asp Asn Val Thr Trp Ser Ala Arg Gly Thr Asp Asn Asn
 305 310 315 320
 Pro Ala Gly Pro Asp Pro Gln Ser Asn Thr Thr Val Ser Ile Pro Tyr
 325 330 335
 Ala Phe Ser Leu Asp Pro Ala Thr Cys Val Pro Asp Val Val Ser Arg
 340 345 350
 Thr Ala Gly Ala Gly Lys Gly Leu Gln Val Ser Asn Gly Ser Cys Ser
 355 360 365
 Pro Gln Thr Pro Thr Pro Thr Thr Gly Thr Pro Thr Thr Pro Ala
 370 375 380
 Pro Thr Thr Pro Thr Pro Ser Pro Thr Pro Ser Thr Pro Gly Pro Thr
 385 390 395 400
 Gln Pro Gly Gly Thr Asn Leu Ser Ile Gly Ala Gly Ser Asp Gly Ser
 405 410 415
 Ser Lys Ala Asp Gly Thr Ser Tyr Gly Asn Val Arg Asp Gly Asp Leu
 420 425 430
 Gly Thr His Trp Ser Pro Ala Gly Ser Thr Gly Ser Val Ser Ile Lys
 435 440 445
 Trp Gly Ser Ala Thr Thr Val Ser Arg Ile Val Ile Arg Glu Ala Ala
 450 455 460
 Gly Ala Thr Gly Val Ile Gly Ser Trp Leu Val Leu Asn Gly Asp Thr
 465 470 475 480
 Gly Ala Val Leu Thr Ser Gly Ser Gly Ala Gly Thr Ile Ser Val Pro
 485 490 495
 Arg Thr Ala Leu Lys Lys Ile Thr Phe Glu Ile Thr Gly Ala Ser Gly
 500 505 510
 Thr Pro Arg Ile Ala Glu Phe Glu Thr Tyr Ala Gly
 515 520

<210> 17

<211> 1047

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 17

ttgccgcgtg	cgcccgggtg	tgagtcgtca	tcgccagcgc	agacgtcatc	ggttgcggtc	60
tcctgggatc	agatcctccg	tcagcctgcg	gcctgggtacg	gcggtgcgga	ggcgttgcca	120
gtcgtgaga	acgtgtcttt	gtatcagcgc	gcggcaggag	ggtggccgaa	gaacatcaac	180
atggcggcgc	cgatgaccgc	cgctgaccgt	gcgaaagtca	cggacgagcg	cgcgcagAAC	240
gacgccacga	tcgacaacac	gtcaacgacg	acgcagatcc	gttttcttgc	gtcgtgtctt	300
cgcggcaccg	ccgacgcacg	attcaaggac	gcggcgctga	agggcatcga	cttcctgctg	360
gctgcgcaat	acgcgaatgg	aggctggcct	cagtattttc	ccctgcgcga	cgactactcg	420
cggcgcatac	cgttcaatga	cgacgcgatg	gtgaatgtga	tgacgtgct	gcgcgagact	480
tcgcagggcc	agacgcggtt	cgagttcgtc	gacgcctcgc	ggcgcggccg	ggcggcgag	540
tctgtctcac	gcggcgctga	cgatcatgctg	cgcacgcaga	ttcgagtcaa	cgcggtgctg	600
accggctggt	gccagcagca	cgacgagcgg	aactttcagc	cggtgaaggc	gcgcgcgtac	660
gaacatccgt	cgattgccag	caaggaaacc	gcgagcatcg	caagattcct	gatggggatt	720
gaacggccgt	cgccggagat	cgtgtccgcg	gtggatggcg	cagtcgcggtg	ggtgcgagcg	780
gcgcagattt	caggtgtgcg	gacggagcgc	cggcccagacg	gatcgaatcc	ggcgggcgac	840
gtcgtggcgg	tgcaggactc	cgccgcgccg	ccaatctggg	cccgttcta	cgagattggc	900
accaaccggc	cgatgttttc	gggtcgcgac	ggcgtcatca	agtacagcct	cagcgagatc	960
gagatcgagc	ggcgcgctgg	atacagctgg	tacggcgact	acgccgccag	actgctcaga	1020

gacgactatc cgaagtggaa gaaatga

1047

<210> 18
 <211> 348
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(348)
 <223> Catalytic domain

<400> 18
 Met Pro Arg Ala Pro Gly Gly Glu Ser Ser Ser Pro Ala Gln Thr Ser
 1 5 10 15
 Ser Val Ala Val Ser Trp Asp Gln Ile Leu Arg Gln Pro Ala Ala Trp
 20 25 30
 Tyr Gly Gly Ala Glu Ala Leu Arg Val Ala Glu Asn Val Leu Leu Tyr
 35 40 45
 Gln Arg Ala Ala Gly Gly Trp Pro Lys Asn Ile Asn Met Ala Ala Pro
 50 55 60
 Met Thr Ala Ala Asp Arg Ala Lys Val Thr Asp Glu Arg Ala Gln Asn
 65 70 75 80
 Asp Ala Thr Ile Asp Asn Thr Ser Thr Thr Thr Gln Ile Arg Phe Leu
 85 90 95
 Ala Leu Val Leu Arg Gly Thr Ala Asp Ala Arg Phe Lys Asp Ala Ala
 100 105 110
 Leu Lys Gly Ile Asp Phe Leu Leu Ala Ala Gln Tyr Ala Asn Gly Gly
 115 120 125
 Trp Pro Gln Tyr Phe Pro Leu Arg Asp Asp Tyr Ser Arg Arg Ile Thr
 130 135 140
 Phe Asn Asp Asp Ala Met Val Asn Val Met Thr Leu Leu Arg Glu Thr
 145 150 155 160
 Ser Gln Gly Gln Thr Pro Phe Glu Phe Val Asp Ala Ser Arg Arg Gly
 165 170 175
 Arg Ala Ala Gln Ser Val Ser Arg Gly Val Asp Val Met Leu Arg Thr
 180 185 190
 Gln Ile Arg Val Asn Gly Val Leu Thr Gly Trp Cys Gln Gln His Asp
 195 200 205
 Glu Arg Asn Phe Gln Pro Val Lys Ala Arg Ala Tyr Glu His Pro Ser
 210 215 220
 Ile Ala Ser Lys Glu Thr Ala Ser Ile Ala Arg Phe Leu Met Gly Ile
 225 230 235 240
 Glu Arg Pro Ser Pro Glu Ile Val Ser Ala Val Asp Gly Ala Val Ala
 245 250 255
 Trp Leu Arg Ala Ala Gln Ile Ser Gly Val Arg Thr Glu Arg Arg Pro
 260 265 270
 Asp Gly Ser Asn Pro Gly Gly Asp Val Val Ala Val Gln Asp Ser Ala
 275 280 285
 Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro
 290 295 300
 Met Phe Ser Gly Arg Asp Gly Val Ile Lys Tyr Ser Leu Ser Glu Ile
 305 310 315 320
 Glu Ile Glu Arg Arg Ala Gly Tyr Ser Trp Tyr Gly Asp Tyr Ala Ala
 325 330 335
 Arg Leu Leu Arg Asp Asp Tyr Pro Lys Trp Lys Lys
 340 345

<210> 19
 <211> 1122
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 19
 gtgaacaggt ggcgcaaga cttcttgccg gacttcgcgg cccgcatgct ccggtgcatg 60
 gttccccggc cgcatatcca ctggggcggc ggtgtcatcc ggcaggaacc ggaatggtag 120
 ggctcggccg aggcgcgtgc gatcgccgac agcgttcttc aataccagtc gaccgctggc 180
 ggctggccca agaaccacca cttgacggtc tcgccaccgt ccgccgaatt ccttgccgat 240
 gcggatggtc tcacgaacac gatcgacaac gacgccacca cgttgccgat gcgatttctc 300
 gctctggtgg cgacgcgcac cggcggcatc aagtaccgcg ccgcgttcga acgcggtctg 360
 gactacctgc tcgccgtca gtatcccaat ggcggctggc ctccagtattt tcccctgcgt 420
 gacggctatt actcgacat cacctacaac gacaatgcga tggtaacgt cctcaccgtt 480
 ctgcgcgatg cggccgcggg ccggccccct tactcgttcg tcgacagggc ccggcgcgcc 540
 agagcagaaa cggccatcgc tcgcggcatc gacatcatcg tgcgactca ggtgagacgg 600
 gccggcgtgc tgaccatgc gtgcgccag cagcagaaa agacgctcga gccggcgtgg 660
 gcgcgcaact acgaaccgcc gacactctcc gggcagaaa gcgtcggcat cgtgcgcttt 720
 ctcatgggaa tcgaaaagcc cagcccgagg atcgtcgcgg cggtgcaagg cgccgctgac 780
 tggttgagag ccgtcgcgat cagcgggttg cgtctcagg aattcaccga cgccgatggc 840
 aggcgcgaca ggcgcgtcgt cgccgatccg gcagcgcgc tcctgtgggc gcgcttctac 900
 gagcttgga cggaccgtcc cgtcttcacc ggccgcgaca aggtgatccg gtactcgctc 960
 agcgaatcgc agcagagcg ccggaacggg tatgcctact atggcacatg gccggccacg 1020
 ctccctcagc aggagtaccc ccgttgccgc gcgaaacacc tggctcgacg gagcgtcagg 1080
 caggtagagg agggaatcgc gatacgcgtc cctaaccct ga 1122

<210> 20
 <211> 373
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(373)
 <223> Catalytic domain

<400> 20
 Met Asn Arg Trp Arg Glu Asp Phe Leu Arg Asp Phe Ala Ala Arg Met
 1 5 10 15
 Leu Arg Cys Met Val Pro Arg Pro Gln Ile His Trp Gly Gly Gly Val
 20 25 30
 Ile Arg Gln Glu Pro Glu Trp Tyr Gly Ser Ala Glu Ala Arg Ala Ile
 35 40 45
 Ala Asp Ser Val Leu Gln Tyr Gln Ser Thr Ala Gly Gly Trp Pro Lys
 50 55 60
 Asn Thr Asp Leu Thr Val Ser Pro Pro Ser Ala Glu Phe Leu Ala Asp
 65 70 75 80
 Ala Asp Gly Leu Thr Asn Thr Ile Asp Asn Asp Ala Thr Thr Leu Pro
 85 90 95
 Met Arg Phe Leu Ala Leu Val Ala His Ala Thr Gly Gly Ile Lys Tyr
 100 105 110
 Arg Ala Ala Phe Glu Arg Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
 115 120 125

Pro Asn Gly Gly Trp Pro Gln Tyr Phe Pro Leu Arg Asp Gly Tyr Tyr
 130 135 140
 Ser His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Val
 145 150 155 160
 Leu Arg Asp Ala Ala Gly Arg Pro Pro Tyr Ser Phe Val Asp Arg
 165 170 175
 Ala Arg Arg Ala Arg Ala Glu Thr Ala Ile Ala Arg Gly Ile Asp Ile
 180 185 190
 Ile Val Arg Thr Gln Val Arg Arg Ala Gly Val Leu Thr Ala Trp Cys
 195 200 205
 Ala Gln His Asp Glu Lys Thr Leu Glu Pro Ala Trp Ala Arg Asn Tyr
 210 215 220
 Glu Pro Pro Thr Leu Ser Gly His Glu Ser Val Gly Ile Val Arg Phe
 225 230 235 240
 Leu Met Gly Ile Glu Lys Pro Thr Pro Arg Ile Val Ala Ala Val Gln
 245 250 255
 Gly Ala Ala Asp Trp Leu Arg Ala Val Ala Ile Ser Gly Leu Arg Leu
 260 265 270
 Glu Glu Phe Thr Asp Ala Asp Gly Arg Arg Asp Arg Val Val Ala
 275 280 285
 Asp Pro Ala Ala Pro Leu Leu Trp Ala Arg Phe Tyr Glu Leu Gly Thr
 290 295 300
 Asp Arg Pro Val Phe Thr Gly Arg Asp Lys Val Ile Arg Tyr Ser Leu
 305 310 315 320
 Ser Glu Ile Glu His Glu Arg Arg Asn Gly Tyr Ala Tyr Tyr Gly Thr
 325 330 335
 Trp Pro Ala Thr Leu Leu Ser Glu Glu Tyr Pro Arg Trp Arg Ala Lys
 340 345 350
 His Leu Ala Arg Arg Ser Val Arg Gln Val Glu Glu Gly Ile Ala Ile
 355 360 365
 Arg Val Pro Asn Pro
 370

<210> 21

<211> 1269

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 21

atgcgtaaat	cgaactgggc	cgtcacaacg	gccatcctgc	tcgcgctgag	cgccgcaccg	60
ctggcgggcaa	agcccatcgg	acagatcacc	ctcgcgctgc	cgctcagccc	ggcgcgctg	120
accgaaacgc	cgcttgagca	gcgggcgcaa	tggcaggcct	atctcgccac	caccgaggca	180
cagcttaagg	cagacaaggc	ggcgctggct	gccgagcgcg	ccggtctggc	cgaaatcccc	240
gccaagccga	agaccggcag	cgccaacacc	atgccgctcg	acaagccgct	ggaatggtac	300
gcgtcggtccg	aggcgcgctct	ggtcgccgat	aatatcgtea	gctatcagac	tccggcaggc	360
ggctggggca	aaaatcaggc	ccgcaacgaa	cccacgcggg	tgaaaggtea	ggcctacact	420
atcgatgacg	ccgatcccac	cggttcgggc	aaatggaact	tcgtcggcac	catcgacaac	480
gacgccacca	tcgtggaaat	tcgctttctc	gcccgcgtag	cggcgggcgg	cacggggccc	540
gaaggcgacg	tctatcgcg	ctccgccacg	cgcgcatca	cctacttgct	ggcgggcgag	600
taccccaatg	gcggctggcc	gcaggctctg	ccgcttcagg	gcggctatca	cgacgccatc	660
accctcaatg	acggcgcgat	gatccatgtg	ctcgaactgt	ttgacgacat	cgccagcgga	720
cagggcgact	tcgccttcct	gcctgagccg	ctgcgcgaca	aggtcgaggc	cgcacaggca	780
aagggtcaga	agggtgcttct	cgatcttcag	cttaagcgca	acggcgaacg	caccctgtgg	840
gcgcagcagt	acgatccgat	taccctcttg	cccagcgcg	cgcgtaacta	cgagccgtcg	900
tcgatcagca	ccggtgaaag	cgccggtgtg	ctgatctacc	tcatgtccct	gcccgaaccc	960
tcgcctgaag	tgcgcgacgc	catcgaaaaa	ggcgtggccc	tgctgatcaa	acttcagatc	1020

```

aacggcatgg catgggaaaa ggacggcatg cgcaaacgtc tggtcgcaa ggctgacgcc 1080
tcgccgctgt ggtcgcgcta tcacgactcg gaaacgctgc tgcccatctt cggtgaccgc 1140
gacatgcgca tcttcgacga cgtcaacgac atcagcgacg aacgcagccg cggctatgcc 1200
tggtatggca caagcccggc acggggccatc gccgaatacg aaaaatggaa acagggcaac 1260
ggcaaatga 1269

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<210> 22
<211> 422
<212> PRT
<213> Unknown

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<220>
<223> Obtained from an environmental sample

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<221> SIGNAL
<222> (1)...(23)

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```

<221> DOMAIN
<222> (24)...(422)
<223> Catalytic domain

```

```

<400> 22
Met Arg Lys Ser Asn Trp Ala Val Thr Thr Ala Ile Leu Leu Ala Leu
 1          5          10          15
Ser Ala Ala Pro Leu Ala Ala Lys Pro Ile Gly Gln Ile Thr Leu Ala
 20          25          30
Val Pro Leu Ser Pro Ala Arg Leu Thr Glu Thr Pro Pro Glu Gln Arg
 35          40          45
Ala Gln Trp Gln Ala Tyr Leu Ala Thr Thr Glu Ala Gln Leu Lys Ala
 50          55          60
Asp Lys Ala Ala Leu Ala Ala Glu Arg Ala Gly Leu Ala Glu Ile Pro
 65          70          75          80
Ala Lys Pro Lys Thr Gly Ser Ala Asn Thr Met Pro Leu Asp Lys Pro
 85          90          95
Leu Glu Trp Tyr Ala Ser Ser Glu Ala Arg Leu Val Ala Asp Asn Ile
100          105          110
Val Ser Tyr Gln Thr Pro Ala Gly Gly Trp Gly Lys Asn Gln Ala Arg
115          120          125
Asn Glu Pro Thr Arg Leu Lys Gly Gln Ala Tyr Thr Ile Asp Asp Ala
130          135          140
Asp Pro Thr Gly Ser Gly Lys Trp Asn Phe Val Gly Thr Ile Asp Asn
145          150          155          160
Asp Ala Thr Ile Val Glu Ile Arg Phe Leu Ala Arg Val Ala Ala Ala
165          170          175
Ala Thr Gly Pro Glu Gly Asp Val Tyr Arg Ala Ser Ala Thr Arg Gly
180          185          190
Ile Thr Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln
195          200          205
Val Trp Pro Leu Gln Gly Gly Tyr His Asp Ala Ile Thr Leu Asn Asp
210          215          220
Gly Ala Met Ile His Val Leu Glu Leu Phe Asp Asp Ile Ala Ser Gly
225          230          235          240
Gln Gly Asp Phe Ala Phe Leu Pro Glu Pro Leu Arg Asp Lys Val Glu
245          250          255
Ala Ala Gln Ala Lys Gly Gln Lys Val Leu Leu Asp Leu Gln Leu Lys
260          265          270
Arg Asn Gly Glu Arg Thr Leu Trp Ala Gln Gln Tyr Asp Pro Ile Thr
275          280          285
Leu Leu Pro Ser Ala Ala Arg Asn Tyr Glu Pro Ser Ser Ile Ser Thr

```

290		295		300
Gly Glu Ser Ala Gly Val Leu Ile Tyr Leu Met Ser Leu Pro Asn Pro				
305		310		315
Ser Pro Glu Val Arg Asp Ala Ile Glu Lys Gly Val Ala Leu Leu Ile				
	325		330	
Lys Leu Gln Ile Asn Gly Met Ala Trp Glu Lys Asp Gly Met Arg Lys				
	340		345	
Arg Leu Val Ala Lys Ala Asp Ala Ser Pro Leu Trp Ser Arg Tyr His				
	355		360	
Asp Ser Glu Thr Leu Leu Pro Ile Phe Gly Asp Arg Asp Met Arg Ile				
	370		375	
Phe Asp Asp Val Asn Asp Ile Ser Asp Glu Arg Ser Arg Gly Tyr Ala				
385		390		395
Trp Tyr Gly Thr Ser Pro Ala Arg Ala Ile Ala Glu Tyr Glu Lys Trp				
	405		410	
Lys Gln Gly Asn Gly Lys				
	420			

<210> 23
 <211> 1182
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 23	
atgaaccgtg gcggtgattgt tttgctggcg gccgctccag ctgcggcgca tggcgagtg	60
ctggggtata tgacgcctgc gcagcggtg accgaggcgc gcattgccgc gctgccggcg	120
tcggagcagg gcgcctggcg gggctacct gcccgctccc gcgcagccat ggacgccgac	180
aaggccgccc tggccgcca gcgcgcgcgc ctgccaccg taccgccggc gccgccgcat	240
ggcggtggtg atggcgggat ggcgcgcaac cgtccgacgg cttggtatgg gacgccgaa	300
gcgcggcaca tcgcggacaa tatcgtcagc ttccagacgc cgtccggcgg ctggggcaag	360
aacgtggacc gcacgggacc tgtgcgccag cgcggacagc attacgttc cttcgatggc	420
aaggagtcc tgaacttcat cggcacgac gacaacaacg ccacaacgag cgagctgaaa	480
ttcctggcgc gcgtgcaggc gcaaatgccc ggcgcgcgcg gcgacgaata ccggaaggcc	540
gccctgcgcg gcatcagcta cctgttgaac tcacaatat ccaacggcgg cttcccgcag	600
gtctatccgc tgcaaggcgg ctaccacgac gccatcacct tcaacgacga tgccttcgcc	660
aacgtgctgc aagtgtgct ggaagtggcg aaccgcagg gcgactatgc cttcgtcccc	720
gaaaccgtgg caaccgatgc ccgcgcggcc gcggacaagg cgctccaagt cctgctggcg	780
agccagatca tcgtcggcgg cgtacgcacc gcctggtgcc agcagcacga tgcgatcacg	840
ctggcgcccc tcggcgcccc caatttcgaa ccggccgcgc tgaccagcac ggaaagcgcg	900
cgctgtctga tgcgttgat gctgctgcc gatccgagcc cggagctgag agcgtcaatc	960
catgcgggga tggcctggct gcagaaagcg gcgctgccgg gggatgtctg gtcgcgctac	1020
tatgacctga acacgatgag gccgatcttt ggggatcgtg accgcagtat ccacgatgat	1080
gtgaaggaat tgagcgagga gaggcaaaaa ggctatggct ggttcagtaa cggaccagcc	1140
agagctaaac aggttttga ggctggacg cgaaacctt ga	1182

<210> 24
 <211> 393
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(18)

<221> DOMAIN

<222> (19)...(393)

<223> Catalytic domain

<400> 24

```

Met Asn Arg Gly Val Ile Val Leu Leu Ala Ala Ala Pro Ala Ala Ala
 1              5              10              15
His Gly Ala Val Leu Gly Tyr Met Thr Pro Ala Gln Pro Leu Thr Glu
              20              25              30
Ala Arg Ile Ala Ala Leu Pro Ala Ser Glu Gln Gly Ala Trp Arg Gly
              35              40              45
Tyr Leu Ala Arg Ser Arg Ala Ala Met Asp Ala Asp Lys Ala Ala Leu
 50              55              60
Ala Ala Glu Arg Ala Ala Leu Ala Thr Val Pro Ala Pro Pro His
 65              70              75              80
Gly Gly Gly Asp Gly Gly Met Ala Arg Asn Arg Pro Thr Ala Trp Tyr
              85              90              95
Gly Thr Pro Glu Ala Arg His Ile Ala Asp Asn Ile Val Ser Phe Gln
              100             105             110
Thr Pro Ser Gly Gly Trp Gly Lys Asn Val Asp Arg Thr Gly Pro Val
              115             120             125
Arg Gln Arg Gly Gln His Tyr Val Ser Phe Asp Gly Lys Glu Ser Trp
 130             135             140
Asn Phe Ile Gly Thr Ile Asp Asn Asn Ala Thr Thr Ser Glu Leu Lys
 145             150             155             160
Phe Leu Ala Arg Val Gln Ala Gln Met Pro Gly Ala Ala Gly Asp Glu
              165             170             175
Tyr Arg Lys Ala Ala Leu Arg Gly Ile Ser Tyr Leu Leu Asn Ser Gln
              180             185             190
Tyr Pro Asn Gly Gly Phe Pro Gln Val Tyr Pro Leu Gln Gly Gly Tyr
              195             200             205
His Asp Ala Ile Thr Phe Asn Asp Asp Ala Phe Ala Asn Val Leu Gln
 210             215             220
Val Leu Leu Glu Val Ala Asn Arg Arg Gly Asp Tyr Ala Phe Val Pro
 225             230             235             240
Glu Thr Val Ala Thr Asp Ala Arg Ala Ala Ala Asp Lys Ala Leu Gln
              245             250             255
Val Leu Leu Ala Ser Gln Ile Ile Val Gly Gly Val Arg Thr Ala Trp
 260             265             270
Cys Gln Gln His Asp Ala Ile Thr Leu Ala Pro Val Gly Ala Arg Asn
 275             280             285
Phe Glu Pro Ala Ala Leu Thr Ser Thr Glu Ser Ala Arg Leu Leu Met
 290             295             300
Leu Leu Met Leu Leu Pro Asp Pro Ser Pro Glu Leu Arg Ala Ser Ile
 305             310             315             320
His Ala Gly Met Ala Trp Leu Gln Lys Ala Ala Leu Pro Gly Asp Val
              325             330             335
Trp Ser Arg Tyr Tyr Asp Leu Asn Thr Met Arg Pro Ile Phe Gly Asp
              340             345             350
Arg Asp Arg Ser Ile His Asp Asp Val Lys Glu Leu Ser Glu Glu Arg
              355             360             365
Gln Lys Gly Tyr Gly Trp Phe Ser Asn Gly Pro Ala Arg Ala Lys Gln
 370             375             380
Ala Phe Glu Ala Trp Thr Arg Lys Pro
 385             390

```

<210> 25

<211> 1194

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 25

```

ttggtcgctg ccctattaag ctgcggcagc gccaatctct atgcagaatc aaccgcaaaa      60
tcggttacgc aatcagcagc cacaaatcaa ttgcaaatg aaaaaagcag ttgggacagc      120
tattacgccg catccaaaaa aatacatcag gcagaccagg attttctcgc cgctgaatta      180
aaaaaactcg gtcagaaaaa accaacattg cccgcacaca ccaaagattt tggttttgat      240
gttaagcagg taaatgcaga ttggttttaa agtgacgaag gcaaacgtgt gatggagatt      300
attctctcct tccaaacccc gtccggcggg ttgtcaaagc gtaccgacat ggccaaggcg      360
gtgcgacaac ctgggcaagc ctttggcgtt gaaaaaggct atatcccaac atttgataat      420
ggcgctacca gcactcaatt gatgttgctc gcgcaagcac accaagccac cggcgatcac      480
cgcttttagcg acgcattttg gcgcggcgtt caattaattt tgactgcgca ataccggaat      540
ggtggctggc caaaaaactt tccactaacc ggtagctacc acgattacat cacctacaac      600
gacaatctta cgcgcgacct gatggtagtg ctgcacaaaa cagcgcaggc aaaaaatgat      660
tttgcatctg tgaccaaaagc gcagcaaadc gcagcgtcag ctagcctcgc gcgtgcactt      720
gattgcgtat tgaaatcaca agttgtcgtc aatggcacac gcacactctg gggcgcacag      780
cacgatgtta aaacactgca accaaccaaa gcgcgcgcac ttgaaatggg gtcactcact      840
accactgaaa gcgcagccat gctcagtttt ctgatggata tcaaaaatcc cagcgcggat      900
attattcaat ccatacatgc agccatagcc tggatatgagc aaaataaaat cgtcggaaaa      960
acctggacac gtggtgatgc ggaattaaaa gataataaaa attcgcagcc actctgggcg     1020
cgtttttatg agataggcac taataagcct atatttgggg atcgcgatga cactgtgtat     1080
tacgatttgg caaaagtgtc taaagagcgt cgcgaagggt atgcgtggta ctccactgac     1140
ccgaataaga cgctaaaaaa atatgctgaa tgggtctaaaa aatatcccaa ataa         1194

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<210> 26

<211> 397

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(15)

<221> DOMAIN

<222> (16)...(397)

<223> Catalytic domain

<400> 26

```

Met Val Ala Ala Leu Leu Ser Cys Gly Ser Ala Asn Leu Tyr Ala Glu
  1           5           10           15
Ser Thr Ala Lys Ser Val Thr Gln Ser Ala Ala Thr Asn Gln Leu Gln
          20          25          30
Asn Glu Lys Ser Ser Trp Asp Ser Tyr Tyr Ala Ala Ser Lys Lys Ile
          35          40          45
His Gln Ala Asp Gln Asp Phe Leu Ala Ala Glu Leu Lys Lys Leu Gly
          50          55          60
Gln Lys Lys Pro Thr Leu Pro Ala His Thr Lys Asp Phe Gly Phe Asp
          65          70          75          80
Val Lys Gln Val Asn Ala Asp Trp Phe Lys Ser Asp Glu Gly Lys Arg
          85          90          95
Val Met Glu Ile Ile Leu Ser Phe Gln Thr Pro Ser Gly Gly Trp Ser
          100         105         110
Lys Arg Thr Asp Met Ala Lys Ala Val Arg Gln Pro Gly Gln Ala Phe
          115         120         125

```

Gly	Val	Glu	Lys	Gly	Tyr	Ile	Pro	Thr	Phe	Asp	Asn	Gly	Ala	Thr	Ser		
130						135					140						
Thr	Gln	Leu	Met	Leu	Leu	Ala	Gln	Ala	His	Gln	Ala	Thr	Gly	Asp	His		
145					150					155					160		
Arg	Phe	Ser	Asp	Ala	Phe	Gly	Arg	Gly	Leu	Gln	Leu	Ile	Leu	Thr	Ala		
				165					170						175		
Gln	Tyr	Pro	Asn	Gly	Gly	Trp	Pro	Gln	Asn	Phe	Pro	Leu	Thr	Gly	Ser		
			180					185						190			
Tyr	His	Asp	Tyr	Ile	Thr	Tyr	Asn	Asp	Asn	Leu	Thr	Arg	Asp	Leu	Met		
		195					200					205					
Val	Val	Leu	His	Lys	Thr	Ala	Gln	Ala	Lys	Asn	Asp	Phe	Ala	Phe	Val		
210						215					220						
Thr	Lys	Ala	Gln	Gln	Ile	Ala	Ala	Ser	Ala	Ser	Leu	Ala	Arg	Ala	Leu		
225					230					235					240		
Asp	Cys	Val	Leu	Lys	Ser	Gln	Val	Val	Val	Asn	Gly	Thr	Arg	Thr	Leu		
				245					250						255		
Trp	Gly	Ala	Gln	His	Asp	Val	Lys	Thr	Leu	Gln	Pro	Thr	Lys	Ala	Arg		
			260					265						270			
Ala	Phe	Glu	Met	Val	Ser	Leu	Thr	Thr	Thr	Glu	Ser	Ala	Ala	Met	Leu		
		275					280					285					
Ser	Phe	Leu	Met	Asp	Ile	Lys	Asn	Pro	Ser	Ala	Asp	Ile	Ile	Gln	Ser		
		290				295					300						
Ile	His	Ala	Ala	Ile	Ala	Trp	Tyr	Glu	Gln	Asn	Lys	Ile	Val	Gly	Lys		
305					310					315					320		
Thr	Trp	Thr	Arg	Gly	Asp	Ala	Glu	Leu	Lys	Asp	Asn	Lys	Asn	Ser	Gln		
				325					330						335		
Pro	Leu	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Lys	Pro	Ile	Phe		
			340					345					350				
Gly	Asp	Arg	Asp	Asp	Thr	Val	Tyr	Tyr	Asp	Leu	Ala	Lys	Val	Ser	Lys		
		355					360					365					
Glu	Arg	Arg	Glu	Gly	Tyr	Ala	Trp	Tyr	Ser	Thr	Asp	Pro	Asn	Lys	Thr		
		370				375					380						
Leu	Lys	Lys	Tyr	Ala	Glu	Trp	Ser	Lys	Lys	Tyr	Pro	Lys					
385					390					395							

<210> 27
 <211> 1917
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 27

gtgtctctct	ttagaaaact	cgcactgccg	gttctgtgcg	gtctactgct	ttctgtcgga	60
gcagaaaccc	gagcgtcgaa	gcgcattgtc	gtggccgctg	atggatcggg	tgacgtcagg	120
acgattcaac	aagcgggtgga	ccagggtccc	aaagacaata	cacacccggg	cttgattcag	180
atcaagccgg	gtgtgtatca	ggaacaagtg	cgtgtgcgcc	ccggcaaacg	ctttatcact	240
cttcgcggcg	acgacgcgag	caagaccgtc	atcacctatc	gattgagcgc	actacaagcg	300
ggaaataccc	ggttggcatt	caccacctta	attaatgcag	acgactttcg	cgccgagAAC	360
ctgacgtttg	aaaactcctt	cggcaccggg	tcacaagcgg	ttgctttggt	tgtcgatcgg	420
aaccgcgcga	cgtttgaaaa	ctgccggttc	ctcgggtggc	aggacacttt	gtttgtgaac	480
ggcagccgcc	actttctcaa	agactgctac	gtcgaaggcc	atgtcgattt	cattttcggc	540
acggcctccg	cagtgtttga	gaactgcacc	attcacagca	aaggcgaagg	ttatgtgacc	600
gcgcactatc	gcaccagcga	tgagatggat	accggttttg	tctttcatcg	ttgtcgtttg	660
accggacgag	acacgggccg	cggagtttat	ctcgggaagg	cgtggcgacc	ttacgcgcgc	720
gtcgtcttta	tcgattgtcg	gctggacgca	cacatcagac	ctgaaggctg	ggataattgg	780
agagatccctg	aacgagagaa	gaccgcgtgg	tttgccgagt	acaagtcaaa	agggcccggt	840
gctaattcccg	tagctcgtgt	cgcggtgtcc	aggcagttga	cgacagaaca	agccgccgag	900

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ttttcgcggg aacgcttttt cagccgcgct gttcgcgggc tctctgggca ggccaaccag 960
gcagtcggaa cgatcgcgtg ggacgatgcg cagaaaaaac cgaacgagtg gtatgcgagc 1020
gccgaggcgt tgcgcacgcg cgacaacgtt gttctttatc aacgtgactc cggcggctgg 1080
cccaagaaca tcgacatggg gaagccgctc gacgacaagg gtcgagccgg tcttctgcgc 1140
gtgcgtaaga agaacgattc caccatcgat aacggcgcg cttacacgca actctcgttt 1200
ctagcgcggg tttacacggc gcaaaagcag gagcggcatc gcgagtcgtt tctgaaggga 1260
ctcgattacc tgttgaaggc gcagtatcca aacggaggct ggccgcagtt ctatcccaat 1320
ctcaacggct attacaaaca catcactttc aacgacaacg cgatgatcgg cgtgatgaaa 1380
ctgctgcgcg acgtagcggc agcgaaaccg gcgtatgcgt ttgtcgacga agcacgacga 1440
acgagtgcgg cgaaggcggc gaaaaagga atcgagtgc tactgaagac gcaggtgggt 1500
gtgaatggcc ggcgaccgt gtggtgtgcg caacatgacg aagtcacgct cgcgcctgcc 1560
ccggcgagga cgtttgaatt agtttcgctg agtgggtggtg aaagcgttga gatcgtgcgc 1620
tttttgatgt cgatcaagaa cccgtcgccg gcggttgctg aggcgatcga gtcggcggtt 1680
gcgtggttcg agcaatcgca agtgaaagat cccgcccgcg aacctgcgtg ggcgcgattt 1740
tatgagatcg gcactaatcg tccgatcttc gccgggcgtg acggcgctgt taagtatgat 1800
gtgaaacaga tcgatgagga acgacgaaag aattacgcat ggtacgttga cgacgcagcg 1860
aaactactga agaccgacta tcctgagtgg aaagaaaaga acgccaaga tcaatga 1917

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<210> 28
 <211> 638
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (28)...(308)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (309)...(638)
 <223> Catalytic domain

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<400> 28
Met Ser Leu Phe Arg Lys Leu Ala Leu Pro Val Leu Cys Gly Leu Leu
  1             5             10             15
Leu Ser Val Gly Ala Glu Thr Arg Ala Ser Lys Arg Ile Val Val Ala
  20             25             30
Ala Asp Gly Ser Gly Asp Val Arg Thr Ile Gln Gln Ala Val Asp Gln
  35             40             45
Val Pro Lys Asp Asn Thr His Pro Val Leu Ile Gln Ile Lys Pro Gly
  50             55             60
Val Tyr Gln Glu Gln Val Arg Val Ala Ala Gly Lys Arg Phe Ile Thr
  65             70             75             80
Leu Arg Gly Asp Asp Ala Ser Lys Thr Val Ile Thr Tyr Arg Leu Ser
  85             90             95
Ala Leu Gln Ala Gly Asn Thr Arg Leu Ala Phe Thr Thr Leu Ile Asn
  100            105            110
Ala Asp Asp Phe Arg Ala Glu Asn Leu Thr Phe Glu Asn Ser Phe Gly
  115            120            125
Thr Gly Ser Gln Ala Val Ala Leu Phe Val Asp Ala Asn Arg Ala Thr
  130            135            140
Phe Glu Asn Cys Arg Phe Leu Gly Trp Gln Asp Thr Leu Phe Val Asn
  145            150            155            160
Gly Ser Arg His Phe Phe Lys Asp Cys Tyr Val Glu Gly His Val Asp

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															165						170						175		
Phe	Ile	Phe	Gly	Thr	Ala	Ser	Ala	Val	Phe	Glu	Asn	Cys	Thr	Ile	His														
			180							185				190															
Ser	Lys	Gly	Glu	Gly	Tyr	Val	Thr	Ala	His	Tyr	Arg	Thr	Ser	Asp	Glu														
			195				200				205																		
Met	Asp	Thr	Gly	Phe	Val	Phe	His	Arg	Cys	Arg	Leu	Thr	Gly	Arg	Asp														
			210				215				220																		
Thr	Gly	Arg	Gly	Val	Tyr	Leu	Gly	Arg	Pro	Trp	Arg	Pro	Tyr	Ala	Arg														
225							230				235																		
Val	Val	Phe	Ile	Asp	Cys	Trp	Leu	Asp	Ala	His	Ile	Arg	Pro	Glu	Gly														
			245				250				255																		
Trp	Asp	Asn	Trp	Arg	Asp	Pro	Glu	Arg	Glu	Lys	Thr	Ala	Trp	Phe	Ala														
			260				265				270																		
Glu	Tyr	Lys	Ser	Lys	Gly	Pro	Gly	Ala	Asn	Pro	Val	Ala	Arg	Val	Ala														
			275				280				285																		
Trp	Ser	Arg	Gln	Leu	Thr	Thr	Glu	Gln	Ala	Ala	Glu	Phe	Ser	Arg	Glu														
			290				295				300																		
Arg	Phe	Phe	Ser	Arg	Ala	Val	Arg	Gly	Leu	Ser	Gly	Gln	Ala	Asn	Gln														
305							310				315																		
Ala	Val	Gly	Thr	Ile	Ala	Trp	Asp	Asp	Ala	Gln	Lys	Lys	Pro	Asn	Glu														
			325				330				335																		
Trp	Tyr	Ala	Ser	Ala	Glu	Ala	Leu	Arg	Ile	Ala	Asp	Asn	Val	Val	Leu														
			340				345				350																		
Tyr	Gln	Arg	Asp	Ser	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Gly	Lys														
			355				360				365																		
Pro	Leu	Asp	Asp	Lys	Gly	Arg	Ala	Gly	Leu	Leu	Arg	Val	Arg	Lys	Lys														
			370				375				380																		
Asn	Asp	Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Tyr	Thr	Gln	Leu	Ser	Phe														
385							390				395																		
Leu	Ala	Arg	Val	Tyr	Ala	Gln	Lys	Gln	Glu	Arg	His	Arg	Glu	Ser															
			405				410				415																		
Phe	Leu	Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Lys	Ala	Gln	Tyr	Pro	Asn	Gly														
			420				425				430																		
Gly	Trp	Pro	Gln	Phe	Tyr	Pro	Asn	Leu	Asn	Gly	Tyr	Tyr	Lys	His	Ile														
			435				440				445																		
Thr	Phe	Asn	Asp	Asn	Ala	Met	Ile	Gly	Val	Met	Lys	Leu	Leu	Arg	Asp														
			450				455				460																		
Val	Ala	Ala	Ala	Lys	Pro	Ala	Tyr	Ala	Phe	Val	Asp	Glu	Ala	Arg	Arg														
465							470				475																		
Thr	Ser	Ala	Ala	Lys	Ala	Val	Glu	Lys	Gly	Ile	Glu	Cys	Ile	Leu	Lys														
			485				490				495																		
Thr	Gln	Val	Val	Val	Asn	Gly	Arg	Arg	Thr	Val	Trp	Cys	Ala	Gln	His														
			500				505				510																		
Asp	Glu	Val	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Arg	Thr	Phe	Glu	Leu	Val														
			515				520				525																		
Ser	Leu	Ser	Gly	Gly	Glu	Ser	Val	Glu	Ile	Val	Arg	Phe	Leu	Met	Ser														
			530				535				540																		
Ile	Lys	Asn	Pro	Ser	Pro	Ala	Val	Val	Glu	Ala	Ile	Glu	Ser	Ala	Val														
545							550				555																		
Ala</																													

<210> 29
 <211> 1398
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 29
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 ctcccgcgaac tggcggttcgg acaaaacgat ccctggaaaa ctcaataccc gcagatccctc 120
 gcgcgggatca aaccgccgaa atttccgaag cgcgatttcg tcatcacgaa gttcggcgcg 180
 aaggcgggaa ccgatatgac gcaagcgatc gctaaagccc tcgacgcttg cgcgaaagcc 240
 ggcggcggaac gcgtcgctgt acccgccggc gaatttctca ccggtgcgat ccatctcaag 300
 tcgaacacca atctctacgt ctcaaaaggc gcgactctga agttttcgac cgaccccgaa 360
 aaatatctgc cgatcgttca cacgcggtgg gaagggatgg agttgatgca tctctcgccg 420
 ttcattctacg cgtacgagca gacgaacatc gcgatcaccg gcgagggcac gctcgacggc 480
 caaggcaaatt cgttcttttg gaagtggcac ggcaaccgcg gatacggcgg caaccccgaa 540
 gtgatcagtc agcaaaaagc gcgggcgcgga ctttacgaga tgatggacaa gaacgtaccc 600
 gtcgcggagc gcgtgttcgg tatcgggcac tatctccggc cgcagttcat ccagccgtac 660
 aaatgtaaga acgtcttgat cgaaggcgtg acgatcatcg actcgccgat gtgggaagtt 720
 catccggtgc tttgcgagaa tgtcaccgtc cgcaatcttc acatctcgtc gcacgggtccg 780
 aacaacgacg gctgcgatcc cgagtcgtgc aaagacgtcc tgatcgacaa ctgcttcttc 840
 gacaccgggtg acgactgcat cgcgatcaag tcgggtcgca ataacgacgg tcgtcgctctg 900
 aacacaccga ccgagaacat catcgtccgc aactgcacga tgaaagacgg tcacggtggt 960
 atcacggtcg gaagcgagat ctcgggcggc gtgcgaaact tgttcgacaa cgattgcaag 1020
 atggacagtg cggatctgtg gaccgcgctc cgggtaaaga acaacgcacg gcggggcggc 1080
 atgctggaga atttctattt ccgcaacatc accgtcgggc aagtcgcgcg tgctgtggtc 1140
 gagatcgatt tcaactatga agaaggcgcg aagggatcgt acacaccggt catgcgcaac 1200
 tacgtggtcg aggatctgac gtgcaccagc gggaaccggc ccgtcgatct gcaaggatta 1260
 gacaacgcgc caatttacga tgtgtcgctg cgtaacacga ctttcggcgc gatgaagaac 1320
 aagagcgctg tgaagaatgt ccgaggactg aagatcgaaa acgttaccgt cagcggcacg 1380
 cgcgtggaga gtttatga 1398

<210> 30
 <211> 465
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(27)

<221> DOMAIN
 <222> (77)...(459)
 <223> Catalytic domain

<400> 30
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 Gly Val Ala Val Leu Pro Gln Leu Ala Phe Gly Gln Asn Asp Pro Trp
 20 25 30
 Lys Thr Gln Tyr Pro Gln Ile Leu Ala Arg Ile Lys Pro Pro Lys Phe
 35 40 45
 Pro Lys Arg Asp Phe Val Ile Thr Lys Phe Gly Ala Lys Ala Gly Thr
 50 55 60

Asp	Ser	Thr	Gln	Ala	Ile	Ala	Lys	Ala	Leu	Asp	Ala	Cys	Ala	Lys	Ala	65	70	75	80
Gly	Gly	Gly	Arg	Val	Val	Val	Pro	Ala	Gly	Glu	Phe	Leu	Thr	Gly	Ala	85	90	95	
Ile	His	Leu	Lys	Ser	Asn	Thr	Asn	Leu	Tyr	Val	Ser	Lys	Gly	Ala	Thr	100	105	110	
Leu	Lys	Phe	Ser	Thr	Asp	Pro	Glu	Lys	Tyr	Leu	Pro	Ile	Val	His	Thr	115	120	125	
Arg	Trp	Glu	Gly	Met	Glu	Leu	Met	His	Leu	Ser	Pro	Phe	Ile	Tyr	Ala	130	135	140	
Tyr	Glu	Gln	Thr	Asn	Ile	Ala	Ile	Thr	Gly	Glu	Gly	Thr	Leu	Asp	Gly	145	150	155	160
Gln	Gly	Lys	Ser	Phe	Trp	Lys	Trp	His	Gly	Asn	Pro	Arg	Tyr	Gly		165	170	175	
Gly	Asn	Pro	Glu	Val	Ile	Ser	Gln	Gln	Lys	Ala	Arg	Ala	Arg	Leu	Tyr	180	185	190	
Glu	Met	Met	Asp	Lys	Asn	Val	Pro	Val	Ala	Glu	Arg	Val	Phe	Gly	Ile	195	200	205	
Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro	Tyr	Lys	Cys	Lys	Asn	210	215	220	
Val	Leu	Ile	Glu	Gly	Val	Thr	Ile	Ile	Asp	Ser	Pro	Met	Trp	Glu	Val	225	230	235	240
His	Pro	Val	Leu	Cys	Glu	Asn	Val	Thr	Val	Arg	Asn	Leu	His	Ile	Ser	245	250	255	
Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asp	Pro	Glu	Ser	Cys	Lys	Asp	260	265	270	
Val	Leu	Ile	Asp	Asn	Cys	Phe	Phe	Asp	Thr	Gly	Asp	Asp	Cys	Ile	Ala	275	280	285	
Ile	Lys	Ser	Gly	Arg	Asn	Asn	Asp	Gly	Arg	Arg	Leu	Asn	Thr	Pro	Thr	290	295	300	
Glu	Asn	Ile	Ile	Val	Arg	Asn	Cys	Thr	Met	Lys	Asp	Gly	His	Gly	Gly	305	310	315	320
Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val	Arg	Asn	Leu	Phe	Ala	325	330	335	
His	Asp	Cys	Lys	Met	Asp	Ser	Ala	Asp	Leu	Trp	Thr	Ala	Leu	Arg	Val	340	345	350	
Lys	Asn	Asn	Ala	Ser	Arg	Gly	Gly	Met	Leu	Glu	Asn	Phe	Tyr	Phe	Arg	355	360	365	
Asn	Ile	Thr	Val	Gly	Gln	Val	Ala	Arg	Ala	Val	Val	Glu	Ile	Asp	Phe	370	375	380	
Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Tyr	Thr	Pro	Val	Met	Arg	Asn	385	390	395	400
Tyr	Val	Val	Glu	Asp	Leu	Thr	Cys	Thr	Ser	Gly	Asn	Arg	Pro	Val	Asp	405	410	415	
Leu	Gln	Gly	Leu	Asp	Asn	Ala	Pro	Ile	Tyr	Asp	Val	Ser	Leu	Arg	Asn	420	425	430	
Thr	Thr	Phe	Gly	Ala	Met	Lys	Asn	Lys	Ser	Val	Val	Lys	Asn	Val	Arg	435	440	445	
Gly	Leu	Lys	Ile	Glu	Asn	Val	Thr	Val	Ser	Gly	Thr	Arg	Val	Glu	Ser	450	455	460	
Leu																465			

<210> 31

<211> 1401

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 31

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gtggtctaca	tcccggccgg	acggttcctc	accggtcccc	tccgcctcaa	aagccacgtc	180
cggctccatc	tcgaggccgg	agcgcaactg	ctcttttagtc	aggacccggc	cgattatcct	240
gttctggaga	cgagggtggga	ggggaaggag	gtcttgacct	atgcacacca	gatctacggc	300
gaggacctcg	aaggggtcgc	gattaccggt	cgggggacca	tcgacggccg	gggcgagact	360
tggtggcgac	tcttcgcgc	caaagccttc	acccatcccc	gacccgcct	catcgccctt	420
acccgctgca	aggacatcct	gatagaagga	gtaaccctcg	tcaattcacc	ggcctggacc	480
atcaatcctg	tgatgtgcga	gcgggtgacc	atcgataagg	tgactatcat	caacccgccc	540
gactcgcccc	acaccgacgg	gacgcacccc	gattcctccc	ggaacgtcta	tatcactaac	600
tgctacattg	acgtaggcga	tgactgcata	gccaatcaaag	cgggccgaga	ggactccctt	660
tatcggacgc	cttgtgaaaa	cattgtcatc	gccaactgcc	tcattgcgcca	cggtcacggc	720
ggggtggtca	tcggcagcga	gaccagcggg	ggtattcgca	aggtagtcat	taccaactgc	780
atcttcgagg	acaccgaccg	gggcattaga	cttaagtccc	ggcgcggacg	cggcgggttc	840
gtcgaggacc	tccgggcgac	gaatattatc	atggaaaagg	tgctctgtcc	cttcgtcctc	900
aacatgtact	atgataccgg	gggaggcggtg	atcgacgagc	gcgcgcatga	cttagaacct	960
catccggtaa	gcgaggctac	accctccttc	cgccgcctct	ccttcagtca	cattactgcc	1020
cgggaagtgc	aggccgccgc	ggccttcctc	tacggcctgc	ccgaacagcc	tctggaggac	1080
gtcttatttg	acgatattcg	gatagagctg	gccgccgacg	cttctcctgc	ccgtccggcc	1140
atgatgcggg	ccgtcccgcc	catgagccaa	ggtggtgtgc	tctgctacgg	tgcgcgcgcg	1200
atctccttcc	ggcacatgca	cctccgcggg	caccgcggtc	cgcccttcca	gatcgaacgc	1260
gcggaggcgg	tgcagttgat	gggctgctcg	accgacggca	gtgaagacct	ccagcttgtc	1320
ttgggtcaag	cggaggaggt	caccatccgt	gactgcacct	ttaccgcccc	gcaggacccc	1380
gcaaaagaaa	ggcaaaatta	a				1401

<210> 32

<211> 466

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(348)

<223> Catalytic domain

<400> 32

Met	Ile	Asn	Leu	Tyr	Gly	Val	Phe	Asp	Ile	Arg	Thr	Phe	Gly	Ala	Gln
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Pro	Asp	Gly	Glu	Thr	Pro	Ser	Thr	Ala	Ala	Ile	Thr	Ala	Ala	Ile	Glu
			20					25					30		
Thr	Cys	Ala	Ala	Ala	Gly	Gly	Gly	Val	Val	Tyr	Ile	Pro	Ala	Gly	Arg
		35				40						45			
Phe	Leu	Thr	Gly	Pro	Leu	Arg	Leu	Lys	Ser	His	Val	Arg	Leu	His	Leu
	50				55						60				
Glu	Ala	Gly	Ala	His	Leu	Leu	Phe	Ser	Gln	Asp	Pro	Ala	Asp	Tyr	Pro
65				70					75					80	
Val	Leu	Glu	Thr	Arg	Trp	Glu	Gly	Lys	Glu	Val	Leu	Thr	Tyr	Ala	His
			85					90					95		
Gln	Ile	Tyr	Gly	Glu	Asp	Leu	Glu	Gly	Val	Ala	Ile	Thr	Gly	Arg	Gly
		100					105						110		
Thr	Ile	Asp	Gly	Arg	Gly	Glu	Thr	Trp	Trp	Arg	Leu	Phe	Arg	Ala	Lys
	115					120						125			
Ala	Phe	Thr	His	Pro	Arg	Pro	Arg	Leu	Ile	Ala	Phe	Thr	Arg	Cys	Lys
	130					135						140			

Asp Ile Leu Ile Glu Gly Val Thr Leu Val Asn Ser Pro Ala Trp Thr
 145 150 155 160
 Ile Asn Pro Val Met Cys Glu Arg Val Thr Ile Asp Lys Val Thr Ile
 165 170 175
 Ile Asn Pro Pro Asp Ser Pro Asn Thr Asp Gly Ile Asp Pro Asp Ser
 180 185 190
 Ser Arg Asn Val Tyr Ile Thr Asn Cys Tyr Ile Asp Val Gly Asp Asp
 195 200 205
 Cys Ile Ala Ile Lys Ala Gly Arg Glu Asp Ser Leu Tyr Arg Thr Pro
 210 215 220
 Cys Glu Asn Ile Val Ile Ala Asn Cys Leu Met Arg His Gly His Gly
 225 230 235 240
 Gly Val Val Ile Gly Ser Glu Thr Ser Gly Gly Ile Arg Lys Val Val
 245 250 255
 Ile Thr Asn Cys Ile Phe Glu Asp Thr Asp Arg Gly Ile Arg Leu Lys
 260 265 270
 Ser Arg Arg Gly Arg Gly Gly Phe Val Glu Asp Leu Arg Ala Thr Asn
 275 280 285
 Ile Ile Met Glu Lys Val Leu Cys Pro Phe Val Leu Asn Met Tyr Tyr
 290 295 300
 Asp Thr Gly Gly Gly Val Ile Asp Glu Arg Ala His Asp Leu Glu Pro
 305 310 315 320
 His Pro Val Ser Glu Ala Thr Pro Ser Phe Arg Arg Leu Ser Phe Ser
 325 330 335
 His Ile Thr Ala Arg Glu Val Gln Ala Ala Ala Ala Phe Leu Tyr Gly
 340 345 350
 Leu Pro Glu Gln Pro Leu Glu Asp Val Leu Phe Asp Asp Ile Trp Ile
 355 360 365
 Glu Leu Ala Ala Asp Ala Ser Pro Ala Arg Pro Ala Met Met Arg Ala
 370 375 380
 Val Pro Pro Met Ser Gln Gly Gly Val Leu Cys Tyr Gly Ala Arg Arg
 385 390 395 400
 Ile Ser Phe Arg His Met His Leu Arg Gly His Arg Gly Pro Ala Phe
 405 410 415
 Gln Ile Glu Arg Ala Glu Ala Val Gln Leu Met Gly Cys Ser Thr Asp
 420 425 430
 Gly Ser Glu Asp Pro Gln Leu Val Leu Gly Gln Ala Glu Glu Val Thr
 435 440 445
 Ile Arg Asp Cys Thr Phe Thr Ala Gln Gln Asp Pro Ala Lys Glu Arg
 450 455 460
 Gln Asn
 465

<210> 33
 <211> 1041
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 33
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 cggattacgg ccgacaagat caacaacaag cccgactcct ggcttaccag cgacgaaggc 120
 atcaagctga tcgacaacat catcacctgg cagaaccccg aggggtggctg ggccaagtac 180
 tacgacgcga ccaatccgca caaacaaggc gaagtctacg gcgactggga cggcgtcggc 240
 accatcgaca acggctacac ctacaccgag ctgaatctcc tggcgcacgt ctacaccctc 300
 accaagcgcc cggagatcct cgattcgttc aacaagggcc tggagtttct gctcaaagcc 360
 caatacccca gcggcggtcg gccgcaacgg tttccggtgc ccaacaacta cggcaagtgc 420

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atcacgctca acgacaacgc gatggtgaac gtgatgcagt tcctgcagaa cgtcgcaaag 480
ggcaaggaag acttcgcttt cgtcgacgag cagcgtcgcg ccaaagcgaa ggaggcgttt 540
gaccgcggga tcgactgcct tctgaagctc cagattaccg tgaacggcaa gcttaccgcc 600
tgggcccagc agtatgaccc gaagacactc gcccgggcgc ccgcccgggc gtacgagctc 660
ccgggcctca gcggctgcga aagcgcgccc gtcatgcgct tgttcatgtc tttggagaac 720
cccagtccc aagttcagcg cgcggtccac gcggcgcgcg cttggtacga ggcgtcgaag 780
atcacccggca agaagctggt gcgcgagaac aacgacgtga cactggccga cgacccaac 840
ggcgagccgc tttgggcgcg cttctacgac atcgaaacca accgcccgtt ctattgcggt 900
cgcgacggcg tgaagaagtg gtcgctggac gagatcgagc ccgaacgccg caagggctac 960
gcttgggtcc gccctgggc gacgagcgta ctggagcagt atcgcaagtg ggcggcgaag 1020
caccaccccg tgaacagttg a 1041

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<210> 34
 <211> 346
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(18)

<221> DOMAIN
 <222> (19)...(346)
 <223> Catalytic domain

<400> 34

Met	Lys	Leu	Arg	Cys	Leu	Met	Leu	Thr	Leu	Leu	Leu	Cys	Gly	Ser	Ala
1				5					10					15	
Phe	Ala	Ala	Asp	Arg	Ile	Thr	Ala	Asp	Lys	Ile	Asn	Asn	Lys	Pro	Asp
			20					25					30		
Ser	Trp	Leu	Thr	Ser	Asp	Glu	Gly	Ile	Lys	Leu	Ile	Asp	Asn	Ile	Ile
		35					40					45			
Thr	Trp	Gln	Asn	Pro	Glu	Gly	Gly	Trp	Ala	Lys	Tyr	Tyr	Asp	Ala	Thr
	50					55					60				
Asn	Pro	His	Lys	Gln	Gly	Glu	Val	Tyr	Gly	Asp	Trp	Asp	Gly	Val	Gly
65				70					75					80	
Thr	Ile	Asp	Asn	Gly	Tyr	Thr	Tyr	Thr	Glu	Leu	Asn	Leu	Leu	Ala	His
			85					90						95	
Val	Tyr	Thr	Leu	Thr	Lys	Arg	Pro	Glu	Ile	Leu	Asp	Ser	Phe	Asn	Lys
			100					105					110		
Gly	Leu	Glu	Phe	Leu	Leu	Lys	Ala	Gln	Tyr	Pro	Ser	Gly	Gly	Trp	Pro
		115					120					125			
Gln	Arg	Phe	Pro	Val	Pro	Asn	Asn	Tyr	Gly	Lys	Cys	Ile	Thr	Leu	Asn
	130					135					140				
Asp	Asn	Ala	Met	Val	Asn	Val	Met	Gln	Phe	Leu	Gln	Asn	Val	Ala	Lys
145					150					155					160
Gly	Lys	Glu	Asp	Phe	Ala	Phe	Val	Asp	Glu	Gln	Arg	Arg	Ala	Lys	Ala
			165					170						175	
Lys	Glu	Ala	Phe	Asp	Arg	Gly	Ile	Asp	Cys	Leu	Leu	Lys	Leu	Gln	Ile
		180					185						190		
Thr	Val	Asn	Gly	Lys	Leu	Thr	Ala	Trp	Ala	Gln	Gln	Tyr	Asp	Pro	Lys
		195					200					205			
Thr	Leu	Ala	Ala	Ala	Pro	Ala	Arg	Ala	Tyr	Glu	Leu	Pro	Gly	Leu	Ser
	210					215					220				
Gly	Cys	Glu	Ser	Ala	Pro	Val	Met	Arg	Leu	Phe	Met	Ser	Leu	Glu	Asn
225					230					235				240	
Pro	Ser	Pro	Glu	Val	Gln	Arg	Ala	Val	His	Ala	Ala	Ala	Ala	Trp	Tyr

				245					250					255	
Glu	Ala	Ser	Lys	Ile	Thr	Gly	Lys	Lys	Leu	Val	Arg	Glu	Asn	Asn	Asp
			260					265					270		
Val	Thr	Leu	Ala	Asp	Asp	Pro	Asn	Gly	Glu	Pro	Leu	Trp	Ala	Arg	Phe
		275					280					285			
Tyr	Asp	Ile	Glu	Thr	Asn	Arg	Pro	Phe	Tyr	Cys	Gly	Arg	Asp	Gly	Val
	290					295					300				
Lys	Lys	Trp	Ser	Leu	Asp	Glu	Ile	Glu	Pro	Glu	Arg	Arg	Lys	Gly	Tyr
305					310					315					320
Ala	Trp	Val	Arg	Pro	Trp	Ala	Thr	Ser	Val	Leu	Glu	Gln	Tyr	Arg	Lys
				325					330					335	
Trp	Ala	Ala	Lys	His	Pro	Pro	Val	Asn	Ser						
			340					345							

<210>	35
<211>	1071
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

[illegible]

<210>	36
<211>	356
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

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<221> DOMAIN
<222> (1)...(356)
<223> Catalytic domain
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<400> 36
Met Pro Lys Asn Ser Asp Asp Ala Trp Arg Glu Lys Thr Pro Pro Asp
1 5 10 15
Trp Ser Leu Val Thr Trp Ser Asp Val Phe Lys Gln Lys Pro Leu Trp
20 25 30

Tyr Gln Thr Asp Glu Ala Ala Arg Val Ala Asp Gln Leu Leu Ile Tyr
 35 40 45
 Gln Lys Glu Asn Gly Gly Phe Glu Lys Asn Val Asp Met Ala Leu Met
 50 55 60
 Leu Thr Gln Lys Glu Lys Glu Glu Leu Thr Ala Lys Arg Ser Asp Val
 65 70 75 80
 Ser Glu Thr Thr Ile Asp Asn Arg Thr Thr Tyr Pro Gln Val Ala Tyr
 85 90 95
 Leu Gly Arg Val Ile Thr Ala Ser Leu Leu Lys Pro Ser Pro Pro Ala
 100 105 110
 Asn Leu Pro Lys Tyr Lys Asp Ala Phe Asn Lys Gly Leu Asp Tyr Leu
 115 120 125
 Leu Ala Ser Gln Tyr Glu Asn Gly Gly Phe Pro Gln Phe Tyr Pro Leu
 130 135 140
 Lys Lys Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asp Ala Met Ile
 145 150 155 160
 Gly Val Leu Lys Val Leu Arg Asp Ile Ala Asn Lys Lys Glu Asp Tyr
 165 170 175
 Val Phe Val Asp Glu Ala Arg Arg Leu Arg Ala Glu Gln Ala Val Ala
 180 185 190
 Lys Ala Leu Pro Leu Ile Leu Lys Leu Gln Val Val Val Asp Gly Lys
 195 200 205
 Lys Thr Val Trp Ala Ala Gln Tyr Asp Glu Thr Thr Leu Ala Pro Ala
 210 215 220
 Ala Ala Arg Lys Phe Glu Pro Val Ser Leu Thr Ala Gly Glu Ser Val
 225 230 235 240
 Gly Ile Val Arg Tyr Leu Met Gln Glu Lys Pro Thr Pro Glu Ile Thr
 245 250 255
 Asp Ala Ile Glu Ser Ala Ile Asp Trp Tyr Arg Lys Asn Lys Ile Asp
 260 265 270
 Gly Ile Arg Trp Glu Arg Ile Lys Gly Glu Asn Thr Val Val Lys Asp
 275 280 285
 Lys Ser Ala Pro Pro Ile Trp Ala Arg Phe Tyr Gln Ile Glu Thr Met
 290 295 300
 Arg Pro Ile Phe Ile Gly Arg Asp Ser Val Ile Lys Tyr Asp Val Thr
 305 310 315 320
 Gln Val Glu Ala Glu Arg Arg Asn Gly Tyr Ala Trp Tyr Val Thr Ala
 325 330 335
 Pro Asn Glu Leu Val Asn Glu Asp Tyr Leu Lys Trp Lys Gly Lys Ser
 340 345 350
 Ala Gly Ala Lys
 355

<210> 37

<211> 1860

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 37

atgttcacta	ctactggctc	tcattgcgcc	cggaattccg	cgcggtttttc	ccttactgcg	60
atagcagccg	ctgttgcggt	gatggcaggc	acttcagcat	ttgcagctgc	gacgggtggc	120
ttctctacca	ctgatgggtg	caacgtatcg	ggcgcccgtt	cgtttactgc	atcgacttac	180
cagcaaatca	acaccattat	tgccaacgca	aaactggatg	atgcaggtaa	aaaagtcact	240
gggggtgctt	accgccttat	cattacctac	accggtaatg	aagactcgct	gattaaccag	300
atgatcaaag	accacacggt	gaattcatcg	ggcaactgcc	ctaaccgcgc	ttggagcgaa	360
gcctatcgct	acgtggaaat	taaagagttt	accaagggta	ttaccattca	aggcgcgaa	420

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ggttcttcag caaacttcgg cattgtgatt aataaatctg acaatgtgat tgtgcgtaat 480
atgaaaatcg gtgcgcttgc tgggtgcgagt aacgatgagg atatgattcg tatcgacacc 540
ggcggttaacg tgtggattga tcacaacgaa ttgtttgagg taaataatga atgtaaaggt 600
tcacccgatg gtgacctgac atttgaaagt gcgattgata ttaaaaaagc atcgcaaaat 660
attacggtgt cctacaacat tatccgcgat agtaaaaaag tagggctcga tggttcgagt 720
agcagtgata ttgcaggtgg ccgtaagatt acgttccatc acaatattta tcgcaatgtt 780
gggtgcacgtt taccgttgca acgcggtggg tggacacaca tgtataacaa tctttacgac 840
ggagttacca gctcgggtat taacgttcgt caaggtgggt acgcgctaata cgagaacaac 900
tgggtccaaa atgctgtcaa cccggttacc tgccgttttg acagtagtaa ctgcggttac 960
tgggatctgc gcaacaacaa cgtgcgcaac cctgggtgatt tctccacctt caacattacc 1020
tggaccagcg gtggcaccat cgacgccacc aactggacta ccaactcaacc tttcccgatt 1080
agcattcctt acagctactc gcctgttagc ccgcagtggt tcaaagacaa gttggcaaat 1140
tatgctggtg tcggtaaaaa caatgcgcaa ttaacggcgt ctgctgcag cggaataact 1200
tcatcggtag caccttcacg agtgccagca tcatcgcggt caccttcaag ccgttcaccc 1260
agcagtgca gccaatccag cacaccaact acatcaagct cgagttcagt tgcgcgaacc 1320
ggttcaattt cgctcggtgc aacggcaacc aacaacagca ttgtgttgag ttggtcacc 1380
aacaatgtga cgctcggttc gcaagaagtg tatcgcgata ccgacgtga tccatcgggg 1440
cgtgtgcgta tcgcatccct ggctgcttca gcgcgtatgt ataccgatag cacagcggca 1500
tcgggccaaa cctattacta ctggattaaa aataccactt ctggtgttgt caccaattcc 1560
aatgctgcat cagcgcgtat tggtagcacg gcgtccagtt ctgttgcac aagcagctca 1620
agttcaagcg gcggcgcgcc cgtattaggt ggtactgggt attatccaag cggcttctcc 1680
aagtgcgctg atttgggcgg gacttgttca gtgtcatcgg gcgatggctg ggttgcgttt 1740
ggtcgcaaa gcaagtgggt taccaagaaa gtatcggtag gtagttcaat cgcctgtacc 1800
gttgcgcat ttggttcgga tccacagggc aaccctaaca agtgttctta caaacgttaa 1860

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<210> 38
 <211> 619
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(35)

<221> DOMAIN
 <222> (36)...(387)
 <223> Catalytic domain

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<400> 38
Met Phe Thr Thr Thr Gly Ser His Cys Ala Arg Asn Ser Ala Arg Phe
1      5      10      15
Ser Leu Thr Ala Ile Ala Ala Ala Val Ala Leu Met Ala Gly Thr Ser
20      25      30
Ala Phe Ala Ala Ala Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Asn
35      40      45
Val Ser Gly Ala Arg Ser Phe Thr Ala Ser Thr Tyr Gln Gln Ile Asn
50      55      60
Thr Ile Ile Ala Asn Ala Lys Leu Asp Asp Ala Gly Lys Lys Val Thr
65      70      75      80
Gly Gly Ala Tyr Pro Leu Ile Ile Thr Tyr Thr Gly Asn Glu Asp Ser
85      90      95
Leu Ile Asn Gln Met Ile Lys Asp His Thr Val Asn Ser Ser Gly Asn
100     105     110
Cys Pro Asn Pro Arg Trp Ser Glu Ala Tyr Arg Tyr Val Glu Ile Lys
115     120     125
Glu Phe Thr Lys Gly Ile Thr Ile Gln Gly Ala Asn Gly Ser Ser Ala
130     135     140

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Asn	Phe	Gly	Ile	Val	Ile	Asn	Lys	Ser	Asp	Asn	Val	Ile	Val	Arg	Asn
145					150					155					160
Met	Lys	Ile	Gly	Ala	Leu	Ala	Gly	Ala	Ser	Asn	Asp	Ala	Asp	Met	Ile
				165					170					175	
Arg	Ile	Asp	Thr	Gly	Val	Asn	Val	Trp	Ile	Asp	His	Asn	Glu	Leu	Phe
			180					185					190		
Ala	Val	Asn	Asn	Glu	Cys	Lys	Gly	Ser	Pro	Asp	Gly	Asp	Leu	Thr	Phe
		195					200					205			
Glu	Ser	Ala	Ile	Asp	Ile	Lys	Lys	Ala	Ser	Gln	Asn	Ile	Thr	Val	Ser
	210					215					220				
Tyr	Asn	Ile	Ile	Arg	Asp	Ser	Lys	Lys	Val	Gly	Leu	Asp	Gly	Ser	Ser
225					230					235					240
Ser	Ser	Asp	Ile	Ala	Gly	Gly	Arg	Lys	Ile	Thr	Phe	His	His	Asn	Ile
				245					250					255	
Tyr	Arg	Asn	Val	Gly	Ala	Arg	Leu	Pro	Leu	Gln	Arg	Gly	Gly	Trp	Thr
		260					265						270		
His	Met	Tyr	Asn	Asn	Leu	Tyr	Asp	Gly	Val	Thr	Ser	Ser	Gly	Ile	Asn
	275					280						285			
Val	Arg	Gln	Gly	Gly	Tyr	Ala	Leu	Ile	Glu	Asn	Asn	Trp	Phe	Gln	Asn
	290					295					300				
Ala	Val	Asn	Pro	Val	Thr	Cys	Arg	Phe	Asp	Ser	Ser	Asn	Cys	Gly	Tyr
305					310					315					320
Trp	Asp	Leu	Arg	Asn	Asn	Asn	Val	Arg	Asn	Pro	Gly	Asp	Phe	Ser	Thr
				325					330					335	
Tyr	Asn	Ile	Thr	Trp	Thr	Ser	Gly	Gly	Thr	Ile	Asp	Ala	Thr	Asn	Trp
		340					345						350		
Thr	Thr	Thr	Gln	Pro	Phe	Pro	Ile	Ser	Ile	Pro	Tyr	Ser	Tyr	Ser	Pro
		355					360					365			
Val	Ser	Pro	Gln	Cys	Val	Lys	Asp	Lys	Leu	Ala	Asn	Tyr	Ala	Gly	Val
	370					375					380				
Gly	Lys	Asn	Asn	Ala	Gln	Leu	Thr	Ala	Ser	Ala	Cys	Ser	Gly	Asn	Thr
385					390					395					400
Ser	Ser	Val	Ala	Pro	Ser	Ser	Val	Pro	Ala	Ser	Ser	Ala	Ala	Pro	Ser
				405					410					415	
Ser	Arg	Ser	Ser	Ser	Ser	Ala	Ala	Pro	Ser	Ser	Thr	Pro	Thr	Thr	Ser
		420						425					430		
Ser	Ser	Ser	Ser	Val	Ala	Ala	Thr	Gly	Ser	Ile	Ser	Leu	Gly	Ala	Thr
		435					440					445			
Ala	Thr	Asn	Asn	Ser	Ile	Val	Leu	Ser	Trp	Ser	Pro	Asn	Asn	Val	Thr
	450					455					460				
Leu	Gly	Ser	Gln	Glu	Val	Tyr	Arg	Asp	Thr	Asp	Ala	Asp	Pro	Ser	Gly
465					470					475					480
Arg	Val	Arg	Ile	Ala	Ser	Leu	Ala	Ala	Ser	Ala	Arg	Met	Tyr	Thr	Asp
				485					490					495	
Ser	Thr	Ala	Ala	Ser	Gly	Gln	Thr	Tyr	Tyr	Tyr	Trp	Ile	Lys	Asn	Thr
			500					505					510		
Thr	Ser	Gly	Val	Val	Thr	Asn	Ser	Asn	Ala	Ala	Ser	Ala	Arg	Ile	Gly
		515					520					525			
Ser	Thr	Ala	Ser	Ser	Ser	Val	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Gly
	530					535						540			
Gly	Ala	Pro	Val	Leu	Gly	Gly	Thr	Gly	Asp	Tyr	Pro	Ser	Gly	Phe	Ser
545					550					555					560
Lys	Cys	Ala	Asp	Leu	Gly	Gly	Thr	Cys	Ser	Val	Ser	Ser	Gly	Asp	Gly
				565					570					575	
Trp	Val	Ala	Phe	Gly	Arg	Lys	Gly	Lys	Trp	Val	Thr	Lys	Lys	Val	Ser
			580					585					590		
Val	Gly	Ser	Ser	Ile	Ala	Cys	Thr	Val	Ala	Ala	Phe	Gly	Ser	Asp	Pro
		595					600					605			
Gln	Gly	Asn	Pro	Asn	Lys	Cys	Ser	Tyr	Lys	Arg					

610

615

<210> 39
 <211> 1077
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 39
 atggcgccga tcctccgacc caacctcctt tgcacttacg cgctctgcat gggcttgctc 60
 gccgtggtga gctgcgcggc ggggcccgtg tcagcgcagc agccggcgcc atggagcacg 120
 gccatcgctg agcaggagga gagcgcgttc gcctccccgt cgatgcgcag cgtcgccgac 180
 aacgtcgtgc gccatcagtc ggccgaaggc ggctggccta agaaccacaa tctggcggcg 240
 ccgccatcgg ggccggcgcc ggagggcgtc gccaatacga tcgacaatga tgcgacgacg 300
 ctgccgatgg agtttctggc gcgtgtgatc cagccggcg gcgtccgata caagccggcc 360
 ttcgagcgcg ggctggatta tctgcttgcg gctcagtacg cgaacggcg cggtccgacg 420
 ttctatccgc tgcgcggggg ctattacgat cagtgacgt tcaacgacga cgccatgatc 480
 cgggtgatga ttctgctcgg cgcagtggcg cgcggcgggg cgccctatga atttgtcgac 540
 gccgggcgcc gcgcgcgcgc tgcagccgcg gtcgagcgg gcctggcgct catcctgcgc 600
 acgcagatcc ggccggcgcg ggcgctgacg gtctggtgcg cgcagtatga cagcgccacc 660
 ttgcagcccg cctggggcgcg cgcctatgag ccgccgtccc tgtccggcg gcgaaagtgtg 720
 gggatcgtgc gctatctcat gtcgatcgac catccctcgc ccgaagtcgt cgccgccgtc 780
 gacggcgctg tggcatggct gcgcgcggcc gccattgccg gcgtgcgcgt ggagaatttc 840
 acggacgccg acggccgccc tgaccgccgc gccgtggccg acgcggggcg gccgccgatc 900
 tgggcgcggg tctacgagtt cggcgccaac cggccgatct tcctggggcg tgattccggt 960
 tttcactaca cgttcgaga aatcgagcgc gagcggcgcg caggctacaa ttattacgga 1020
 tactgggcgc gtcctgtgct ggaagactat ccggcctggc gcgcgcgcgt gcgatga 1077

<210> 40
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(32)

<221> DOMAIN
 <222> (33)...(358)
 <223> Catalytic domain

<400> 40
 Met Ala Pro Ile Leu Arg Pro Asn Leu Leu Cys Thr Tyr Ala Leu Cys
 1 5 10 15
 Met Gly Leu Leu Ala Val Val Ser Cys Ala Ala Gly Pro Val Ser Ala
 20 25 30
 Gln Gln Pro Ala Pro Trp Ser Thr Ala Ile Val Glu Gln Glu Glu Ser
 35 40 45
 Ala Phe Ala Ser Pro Ser Met Arg Ser Val Ala Asp Asn Val Val Arg
 50 55 60
 His Gln Ser Ala Glu Gly Gly Trp Pro Lys Asn Thr Asn Leu Ala Ala
 65 70 75 80
 Pro Pro Ser Gly Pro Ala Pro Glu Gly Val Ala Asn Thr Ile Asp Asn
 85 90 95
 Asp Ala Thr Thr Leu Pro Met Glu Phe Leu Ala Arg Val Ile His Ala

[illegible]

<210>	41
<211>	1080
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400> 41							
atgaaaaaatt	taaaatacag	tttagtttca	tttgactact	tcattactat	gaatgttttt		60
acgcaagaaa	aaaaagtaac	ttggaaaagc	atcacagaaa	ataacgatga	aaattgggtt		120
gtaagcggaag	aagccaaaaa	aatagccgaa	aatgttttgt	tatatcaacg	cgatattggg		180
ggttggccaa	aaaacactga	aattcaaaat	gaactttcag	aaaaagaaaa	actaacatta		240
aaagaatttaa	aatcggatcc	aaaaggatgt	accatcgaca	atgggtgcaac	gtgtcaggaa		300
ttacttttct	tatccaaaat	atataaatcc	aatccagatg	agcgatatata	aatggctttc		360
ttaaaagggtg	tgatttacct	gattacagct	caatacaaaa	atgggtggttg	gccacaatat		420
taccctttga	gagaaggata	ttacactcat	attacttaca	acgataatgc	aatgggtgaat		480
gtttttaaagt	tgttgaaaga	agttaaagat	aaatctgatt	actactcaat	tcaagcacc		540
gatgaaattt	ccaaaatggc	tgaagtatca	tttaataaag	gagtcgattg	catattaaaa		600
acacagtaca	aacaaaatgg	aatattaacc	gcttggtgtg	cacaacatga	cagggaaaca		660
ttgaaacctg	ctaaagcaag	agcttatgaa	ttgccttcgt	taagcggaaa	agaattcagc		720
aaaatttgtgt	tgttattaat	gtcaatcgaa	aatccatcta	aagaagtaat	tactgccgta		780
aattcagcag	ttaattgggt	tgaaaaaaca	aaaatcaacg	gaattaaaat	tgaaccatt		840
tccaccggga	aaaaggatga	aaagatatga	attgttggtg	aaagtcctga	tgctccgcg		900
ctttgggcaa	gatttatgga	attaagtgc	aacaaccat	tttttgtga	tcgtgacgga		960

aagaaaaaat acagcatgtc agaaattagt caagagcgta gaaccggcta tgcattggtac 1020
 accaacgaac caaaagaagt tttaaaaaaa tacgatgatt ggaagtcattc attaaactaa 1080

<210> 42
 <211> 359
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(359)
 <223> Catalytic domain

<400> 42
 Met Lys Asn Leu Lys Tyr Ser Leu Val Ser Phe Val Leu Leu Ile Thr
 1 5 10 15
 Met Asn Val Phe Thr Gln Glu Lys Lys Val Thr Trp Lys Ser Ile Thr
 20 25 30
 Glu Asn Asn Asp Glu Asn Trp Phe Val Ser Glu Glu Ala Lys Lys Ile
 35 40 45
 Ala Glu Asn Val Leu Leu Tyr Gln Arg Asp Ile Gly Gly Trp Pro Lys
 50 55 60
 Asn Thr Glu Ile Gln Asn Glu Leu Ser Glu Lys Glu Lys Leu Thr Leu
 65 70 75 80
 Lys Glu Leu Lys Ser Asp Pro Lys Gly Cys Thr Ile Asp Asn Gly Ala
 85 90 95
 Thr Cys Gln Glu Leu Leu Phe Leu Ser Lys Ile Tyr Lys Ser Asn Pro
 100 105 110
 Asp Glu Arg Tyr Lys Met Ala Phe Leu Lys Gly Val Ile Tyr Leu Ile
 115 120 125
 Thr Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Leu Arg
 130 135 140
 Glu Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn
 145 150 155 160
 Val Leu Lys Leu Leu Lys Glu Val Lys Asp Lys Ser Asp Tyr Tyr Ser
 165 170 175
 Ile Gln Ala Pro Asp Glu Ile Ser Lys Met Ala Glu Val Ser Phe Asn
 180 185 190
 Lys Gly Val Asp Cys Ile Leu Lys Thr Gln Tyr Lys Gln Asn Gly Ile
 195 200 205
 Leu Thr Ala Trp Cys Ala Gln His Asp Arg Glu Thr Leu Lys Pro Ala
 210 215 220
 Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu Ser Gly Lys Glu Ser Ala
 225 230 235 240
 Lys Ile Val Leu Leu Leu Met Ser Ile Glu Asn Pro Ser Lys Glu Val
 245 250 255
 Ile Thr Ala Val Asn Ser Ala Val Asn Trp Phe Glu Lys Thr Lys Ile
 260 265 270
 Asn Gly Ile Lys Ile Glu Thr Ile Ser Thr Gly Lys Lys Asp Glu Lys
 275 280 285
 Asp Arg Ile Val Val Glu Ser Pro Asp Ala Pro Pro Leu Trp Ala Arg
 290 295 300
 Phe Met Glu Leu Ser Asp Asn Lys Pro Phe Phe Cys Asp Arg Asp Gly
 305 310 315 320

Lys	Lys	Lys	Tyr	Ser 325	Met	Ser	Glu	Ile	Ser 330	Gln	Glu	Arg	Arg	Thr 335	Gly
Tyr	Ala	Trp	Tyr 340	Thr	Asn	Glu	Pro	Lys 345	Glu	Val	Leu	Lys	Lys 350	Tyr	Asp
Asp	Trp	Lys 355	Ser	Ser	Leu	Asn									

<210>	43
<211>	1902
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	43					
gtggatccaa	agaattggggg	cagcgggattt	accggcgaaa	tcaaagtaac	taacaacaca	60
agccaaacag	tcaatagctg	gtctgtgtca	tggcaagagg	caggagccag	tgtaactaat	120
tcctggaatg	caaccttggg	agggacgaat	ccttataccg	caaccgggtt	aggatggaac	180
tcaaccctgg	cgccccggagc	ctctgccagt	tttggttttc	aagcaaacgg	cactgcgggg	240
gcacaaag	taaatggcag	tttgtgtggg	gcgctgcgat	catctgcagc	gaccagcaaa	300
tccagtgcga	gtgttgccgag	ttcaaagatt	gcaagttcaa	ttcaatcaag	tgcaactagc	360
agttcaaaat	cgtccagttc	tgtctcacct	tcaagcacgc	caaaatccag	tagctctgct	420
ccaacggctg	catcattcac	tattcaagaa	gagcaagccg	gtttttgccg	tgtagacggt	480
attgcaacgg	aaagtaccaa	caccggattc	accggcaacg	gctacaccaa	ttccaataat	540
gtacaagggtg	ctgccattgt	gtgggcggtg	aatgcaacta	ccagtgcacg	ccatacaatt	600
actttccgct	tcgctaattg	tggcattcgc	aatcgcaatg	gctcgctagt	cattaacggc	660
ggcagcaatg	gtaattacac	ggtgcaatta	ccacgcacgg	cgagctgggg	tgactggcaa	720
acagtaaatg	tggaaattga	tttggtagaa	ggcaataaca	atgttgcaact	caccgcattg	780
actgcagatg	gcctcgcaaa	tatcgacttc	atcaaaattg	aaggagcatc	aaccaaagcg	840
ggaacctgtg	caggtgcggt	cagcagtagc	agtgttgctt	cttcggtaaa	atccagtgct	900
agcgcggcaa	gcagttctgt	accaacgaac	accggcgcca	tgctaacttt	ggatggcaac	960
cctgccgcaa	gctggcttaa	caaatcgcgt	acaaagtggg	gcgcatcgcg	cgctgacatt	1020
gtgcctcttt	atcaacagtc	caacggcgcg	tggccaaaaa	atctggatta	caattcagtg	1080
agcgtctggtg	atggcggcag	tgcaagcggc	accatcgata	atgggtgcaac	tattactgaa	1140
atggtttatc	tcgctgaggt	ttacaaaacc	ggaaacaata	ccaagtaccg	cgatgcagtt	1200
cgccgtgcag	caaactttat	cgtgagttcg	caatatagca	ctggcgcggt	gccgcaattt	1260
tatccgctca	aaggtggcta	tgcagaccac	gccaccttta	atgataacgg	catggcttac	1320
gcattaactg	tattggattt	cgctgcaaac	aagcgcgcgc	cttttgatac	ggatgtcttt	1380
aatgacacag	accgcgcaaa	atttaaaaca	gcgtaacca	aaggtgttga	ttacatttta	1440
aaagcgcaat	ggaacaaaaa	tggaaaaatta	acagcctggt	gcgcacaaca	tggcgcgact	1500
gactatcaac	ctaaaaaagc	acgcgcttat	gaattggaat	cactgagtg	tagcgagtct	1560
gttgggtgtg	ttgcattttt	aatgacgcag	ccgcagacag	cacaaatcca	aacggccggt	1620
aaagcaggcc	tcaactgggt	caatagcccc	agcacctatt	tggaagggtg	cacctacgat	1680
tcatccaaag	cgtccactaa	tcccatagtg	cagaaagcgg	gaagtagaat	gtggtatcgc	1740
ttttacgatt	taaatacca	ccgtggtttt	ttcagcgacc	gggacggcag	caaattctat	1800
gacattacca	aaatgtctga	agaacgtcgc	acgggttata	gttggggtgg	cgcttatggt	1860
gagagcatca	tcgccttttg	caaaaaaqtg	qgctatttat	aa		1902

<210>	44
<211>	633
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<221> BINDING
<222> (4) . . . (89)

<223> Carbohydrate binding module

<221> BINDING

$\langle 222 \rangle$ (152) ... (275)

<223> Carbohydrate binding module

<221> DOMAIN

 $\langle 222 \rangle \quad (277) \dots (633)$

<223> Catalytic domain

<400> 44

Met 1	Asp	Pro	Lys	Asn 5	Trp	Gly	Ser	Gly	Phe 10	Thr	Gly	Glu	Ile 15	Lys	Val
Thr	Asn	Asn	Thr	Ser	Gln	Thr	Val	Asn	Ser	Trp	Ser	Val	Ser	Trp	Gln
			20					25					30		
Glu	Ala	Gly	Ala	Ser	Val	Thr	Asn	Ser	Trp	Asn	Ala	Thr	Leu	Gly	Gly
		35					40					45			
Thr	Asn	Pro	Tyr	Thr	Ala	Thr	Gly	Leu	Gly	Trp	Asn	Ser	Thr	Leu	Ala
	50					55					60				
Pro	Gly	Ala	Ser	Ala	Ser	Phe	Gly	Phe	Gln	Ala	Asn	Gly	Thr	Ala	Gly
65					70				75						80
Ala	Pro	Lys	Val	Asn	Gly	Ser	Leu	Cys	Gly	Ala	Thr	Ala	Ser	Ser	Ala
				85					90					95	
Ala	Thr	Ser	Lys	Ser	Ser	Ala	Ser	Val	Ala	Ser	Ser	Lys	Ile	Ala	Ser
			100					105					110		
Ser	Ile	Gln	Ser	Ser	Ala	Thr	Ser	Ser	Ser	Lys	Ser	Ser	Ser	Ser	Ala
		115					120					125			
Ala	Pro	Ser	Ser	Thr	Pro	Lys	Ser	Ser	Ser	Ser	Ala	Pro	Thr	Ala	Ala
	130					135					140				
Ser	Phe	Thr	Ile	Gln	Glu	Gln	Ala	Gly	Phe	Cys	Arg	Val	Asp	Gly	
145				150					155						160
Ile	Ala	Thr	Glu	Ser	Thr	Asn	Thr	Gly	Phe	Thr	Gly	Asn	Gly	Tyr	Thr
			165					170						175	
Asn	Ser	Asn	Asn	Val	Gln	Gly	Ala	Ala	Ile	Val	Trp	Ala	Val	Asn	Ala
			180					185					190		
Thr	Thr	Ser	Ala	Arg	His	Thr	Ile	Thr	Phe	Arg	Phe	Ala	Asn	Gly	Gly
		195				200					205				
Thr	Ala	Asn	Arg	Asn	Gly	Ser	Leu	Val	Ile	Asn	Gly	Ser	Asn	Gly	
	210				215						220				
Asn	Tyr	Thr	Val	Gln	Leu	Pro	Arg	Thr	Ala	Ser	Trp	Ala	Asp	Trp	Gln
225				230						235					240
Thr	Val	Ser	Leu	Glu	Ile	Asp	Leu	Val	Gln	Gly	Asn	Asn	Asn	Leu	Gln
			245						250					255	
Leu	Thr	Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Phe	Ile	Lys
			260					265					270		
Ile	Glu	Gly	Ala	Ser	Thr	Lys	Ala	Gly	Thr	Cys	Ala	Gly	Ala	Val	Ser
		275					280					285			
Ser	Ser	Ser	Val	Ala	Ser	Ser	Val	Lys	Ser	Ser	Ala	Ser	Ala	Ala	Ser
	290					295					300				
Ser	Ser	Val	Pro	Thr	Asn	Thr	Gly	Ala	Met	Leu	Thr	Leu	Asp	Gly	Asn
305				310					315						320
Pro	Ala	Ala	Ser	Trp	Leu	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Ser	Ala	Ser
			325						330					335	
Arg	Ala	Asp	Ile	Val	Ala	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro
			340					345					350		
Lys	Asn	Leu	Asp	Tyr	Asn	Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly		

Ala Glu Val Tyr Lys Thr Gly Asn Asn Thr Lys Tyr Arg Asp Ala Val
 385 390 395 400
 Arg Arg Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala
 405 410 415
 Leu Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr
 420 425 430
 Phe Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala
 435 440 445
 Ala Asn Lys Arg Ala Pro Phe Asp Thr Asp Val Phe Asn Asp Thr Asp
 450 455 460
 Arg Ala Lys Phe Lys Thr Ala Val Thr Lys Gly Val Asp Tyr Ile Leu
 465 470 475 480
 Lys Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln
 485 490 495
 His Gly Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu
 500 505 510
 Glu Ser Leu Ser Gly Ser Glu Ser Val Gly Val Ile Ala Phe Leu Met
 515 520 525
 Thr Gln Pro Gln Thr Ala Gln Ile Gln Thr Ala Val Lys Ala Gly Leu
 530 535 540
 Asn Trp Phe Asn Ser Pro Ser Thr Tyr Leu Glu Gly Tyr Thr Tyr Asp
 545 550 555 560
 Ser Ser Lys Ala Ser Thr Asn Pro Ile Val Gln Lys Ala Gly Ser Arg
 565 570 575
 Met Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser
 580 585 590
 Asp Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Lys Met Ser Glu Glu
 595 600 605
 Arg Arg Thr Gly Tyr Ser Trp Gly Gly Ala Tyr Gly Glu Ser Ile Ile
 610 615 620
 Ala Phe Gly Lys Lys Val Gly Tyr Leu
 625 630

<210> 45

<211> 987

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 45

atgactagac	gcgcccttcac	cgcggttatc	tgtttcttcg	cggccgtctg	cgcgcacgcg	60
cagtcaccg	tgcgtggaa	ggacgtgctc	gagcagtcgc	agggctggta	ttccacgacc	120
gccgcgcacg	tcgtcgccga	cacggtgctg	ctgtatcaac	gtccatccgg	tgatggccg	180
aaggacatcg	acatgacggc	gccgcggcg	gaccgcactc	ctcccgcgcg	tccagacgcg	240
accatcgaca	acggcgccac	gaccacgcag	atccgcctgc	tcgctcgtgc	ggcctcgggc	300
gcaccggcgg	ctgccgccca	cacctacacg	gcggcgggcg	ttcgcgggat	cgattacctg	360
ctcgaggcgc	agtatcccaa	cggcggtctg	ccgcagttct	ttcccctgcg	caaggactat	420
tcgcgtacg	tcacgttcaa	cgacgacgcg	atgatgaacg	tgatgttctt	gctggacgag	480
gtctcggcgg	gagatgcgcc	gttcacgttc	gtggacgaac	aacgccgcga	ccgcgcgcgc	540
gctgccgtcg	ccaaggggt	ctccgtcatc	ctgaagtcgc	aggtccggat	cgacgggacg	600
ctgaccgcct	ggtgcgcgca	acacgacgag	atcaccctgg	caccgcgtcc	ggcgcgcacc	660
ttcgagcacg	cgtcgtctcag	cggcaacgag	tctgtcgcga	tcgtgcgctt	cctgatgacc	720
cgtcgcgcga	cgccagcgat	cgtcgccgcg	gtcgatgcgg	cggtcgcttg	gctcagacgc	780
gtccgcctcc	ctgacggacg	gtgggccgca	ttctacgagt	tcggtaccaa	tcgtccgatc	840
ttctcggggc	gagacagtgt	cgtgcgctac	aaactcgagg	agatcgaaca	ggaacgtcag	900
gagggctacg	cgtggtacgg	cacgtggccg	aggacgcttg	ttgagaagat	gtaccctgca	960
tggaagtgcg	ggcttccggg	caagtag				987

<210> 46
 <211> 328
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(20)

<221> DOMAIN
 <222> (21)...(328)
 <223> Catalytic domain

<400> 46
 Met Thr Arg Arg Ala Phe Ile Ala Val Ile Cys Phe Phe Ala Ala Val
 1 5 10 15
 Cys Ala His Ala Gln Ser Thr Val Arg Trp Lys Asp Val Leu Glu Gln
 20 25 30
 Ser Glu Gly Trp Tyr Ser Thr Thr Ala Ala His Val Val Ala Asp Thr
 35 40 45
 Val Leu Leu Tyr Gln Arg Pro Ser Gly Gly Trp Pro Lys Asp Ile Asp
 50 55 60
 Met Thr Ala Pro Pro Ala Asp Arg Thr Pro Pro Ala Arg Pro Asp Ala
 65 70 75 80
 Thr Ile Asp Asn Gly Ala Thr Thr Thr Gln Ile Arg Leu Leu Ala Arg
 85 90 95
 Ala Ala Ser Gly Ala Pro Ala Ala Ala His Thr Tyr Thr Ala Ala
 100 105 110
 Ala Leu Arg Gly Ile Asp Tyr Leu Leu Glu Ala Gln Tyr Pro Asn Gly
 115 120 125
 Gly Trp Pro Gln Phe Phe Pro Leu Arg Lys Asp Tyr Ser Arg Tyr Val
 130 135 140
 Thr Phe Asn Asp Asp Ala Met Met Asn Val Met Phe Leu Leu Asp Glu
 145 150 155 160
 Val Ser Ala Gly Asp Ala Pro Phe Thr Phe Val Asp Glu Gln Arg Arg
 165 170 175
 Asp Arg Ala Arg Ala Ala Val Ala Lys Gly Val Ser Val Ile Leu Lys
 180 185 190
 Ser Gln Val Arg Ile Asp Gly Thr Leu Thr Ala Trp Cys Ala Gln His
 195 200 205
 Asp Glu Ile Thr Leu Ala Pro Arg Pro Ala Arg Thr Phe Glu His Ala
 210 215 220
 Ser Leu Ser Gly Asn Glu Ser Val Ala Ile Val Arg Phe Leu Met Thr
 225 230 235 240
 Arg Pro Pro Thr Pro Ala Ile Val Ala Ala Val Asp Ala Ala Val Ala
 245 250 255
 Trp Leu Arg Arg Val Arg Leu Pro Asp Gly Arg Trp Ala Arg Phe Tyr
 260 265 270
 Glu Phe Gly Thr Asn Arg Pro Ile Phe Ser Gly Arg Asp Ser Val Val
 275 280 285
 Arg Tyr Lys Leu Glu Glu Ile Glu Gln Glu Arg Gln Glu Gly Tyr Ala
 290 295 300
 Trp Tyr Gly Thr Trp Pro Arg Thr Leu Val Glu Lys Met Tyr Pro Ala
 305 310 315 320
 Trp Lys Ser Arg Leu Pro Gly Lys
 325

<210> 47
 <211> 1077
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 47
 atgaaaaatt ttaaaaaatat ttaggagcg ttacttatat ctgtaacggt ttgtgtgcac 60
 gggcaggtaa acaaaaaatc ctggcgggct attacacagt ctaacgacga tgcattggtt 120
 gcatctgatg gagctgcaca gattgcagat aatgtattac tctatcagcg caatggtggc 180
 ggatggccta aaaatattga aatgcaggaa ccgcttagtg aggccgacaa aaaaaagctg 240
 atagatctta agtctacggc caaagaaagt actacagata atggggctac gtgtcaggaa 300
 atggtattcc tctctaagat atataaaca aagcccgaag agaagtataa agaggctttt 360
 ttaaaaggac ttaattatct gcttgaagca cagtataaaa atgggtggatg gccacagttc 420
 taccctttta aaaaagggtta ttatacccac attacctata atgacgattc tatggtaaac 480
 attcttatga tcttaaagaa tattaaggaa gatgccaaact attacagtat tacgccaaagc 540
 gataaagttt taaagcaggt atcgacagct tttgacagag gcattgactg cattctaaaa 600
 acacagtaca agcaaaaggg tgtgcttaca agctgggtgtg cccagcacga tgagggttaca 660
 ttagaacctg caaatgcaag ggcttttgag ttggcatcac taagtggtaa agaattctgct 720
 aaaataacgt tgttgctaatt gtctgtaaaa aatccgtcta aagaggttgt tgctgctgta 780
 gatgctgctg tggcgtgggt tgaaaaaaca aaaattgaag gcattaaagt agaagaagta 840
 accggagctg atggcaaaaa ggatagggtta gtagtacaaa gggctgatgc cgaaccattg 900
 tgggcgcggt ttatggaaact ggataccaac aggccatttt tttgcgacag ggacggtata 960
 aaaaaatatt cgcttgctga gataggtcat gaacgccgta acggatatgg ctggtacacc 1020
 aacgaaccaa aagaagtttt aaagaaatac accaaatgga aaaacagtct taaatag 1077

<210> 48
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(358)
 <223> Catalytic domain

<400> 48
 Met Lys Asn Phe Lys Asn Ile Val Gly Ala Leu Leu Ile Ser Val Thr
 1 5 10 15
 Phe Cys Val His Gly Gln Val Asn Lys Lys Ser Trp Arg Ala Ile Thr
 20 25 30
 Gln Ser Asn Asp Asp Ala Trp Phe Ala Ser Asp Gly Ala Ala Gln Ile
 35 40 45
 Ala Asp Asn Val Leu Leu Tyr Gln Arg Asn Val Gly Gly Trp Pro Lys
 50 55 60
 Asn Ile Glu Met Gln Glu Pro Leu Ser Glu Ala Asp Lys Lys Lys Leu
 65 70 75 80
 Ile Asp Leu Lys Ser Thr Ala Lys Glu Ser Thr Thr Asp Asn Gly Ala
 85 90 95
 Thr Cys Gln Glu Met Val Phe Leu Ser Lys Ile Tyr Lys Gln Lys Pro
 100 105 110

Glu Glu Lys Tyr Lys Glu Ala Phe Leu Lys Gly Leu Asn Tyr Leu Leu
 115 120 125
 Glu Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu Lys
 130 135 140
 Lys Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Asp Ser Met Val Asn
 145 150 155 160
 Ile Leu Met Ile Leu Lys Asn Ile Lys Glu Asp Ala Asn Tyr Tyr Ser
 165 170 175
 Ile Thr Pro Ser Asp Lys Val Leu Lys Gln Val Ser Thr Ala Phe Asp
 180 185 190
 Arg Gly Ile Asp Cys Ile Leu Lys Thr Gln Tyr Lys Gln Lys Gly Val
 195 200 205
 Leu Thr Ser Trp Cys Ala Gln His Asp Glu Val Thr Leu Glu Pro Ala
 210 215 220
 Asn Ala Arg Ala Phe Glu Leu Ala Ser Leu Ser Gly Lys Glu Ser Ala
 225 230 235 240
 Lys Ile Thr Leu Leu Leu Met Ser Val Lys Asn Pro Ser Lys Glu Val
 245 250 255
 Val Ala Ala Val Asp Ala Ala Val Ala Trp Phe Glu Lys Thr Lys Ile
 260 265 270
 Glu Gly Ile Lys Val Glu Glu Val Thr Gly Ala Asp Gly Lys Lys Asp
 275 280 285
 Arg Val Val Val Gln Arg Ala Asp Ala Glu Pro Leu Trp Ala Arg Phe
 290 295 300
 Met Glu Leu Asp Thr Asn Arg Pro Phe Phe Cys Asp Arg Asp Gly Ile
 305 310 315 320
 Lys Lys Tyr Ser Leu Ala Glu Ile Gly His Glu Arg Arg Asn Gly Tyr
 325 330 335
 Gly Trp Tyr Thr Asn Glu Pro Lys Glu Val Leu Lys Lys Tyr Thr Lys
 340 345 350
 Trp Lys Asn Ser Leu Lys
 355

<210> 49

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 49

atgttaagtt	tcacgcggt	atcagtggtt	cataattact	gcacagggca	gacagcgctc	60
accaaaaatt	cagtggccga	aaagatgctt	cagtaccagt	tgtcaaatgg	cgccctggccc	120
aaacagttgg	tagacaaaag	tgctggtgat	tacagtcttc	cattaacgaa	agagcgccta	180
cagcagatca	agaaaacaga	tattgatcat	gctacgctcg	acaacagtgc	gacaacccgg	240
gaaataactg	aattgatcaa	ggcttttaag	gacactaaaa	ataaggcata	tttgactgct	300
gtagaaaagg	ggattgcata	tattttatcg	gctcaatatg	agaatggcgg	atttccacaa	360
tactacccaa	ataaattata	ctatagagct	gagataacat	acaacgatga	tgcgatgatc	420
aatgcattac	tagtgcttta	caaagtagcc	aataagcgag	aggggtttga	ggctatcaat	480
cccatatttg	tgtcaaaagc	gcaaaaagca	gttgaaaagg	gtataacctg	tatcctaata	540
acacagggtca	tacaagacgg	aaaaaggagt	atttgggctg	cgcaatacga	tcagaacact	600
ttacaacctg	ctcaggcaag	aaagtttgaa	ccagcttcat	tgagcacaag	tgaatctgtt	660
tccatcgctc	gctttctcat	gctacagcct	gcaaccactg	aaattaagca	agcgatcgaa	720
catgcaatac	aatgggtcga	acagcatgat	attgaagggt	accgtttcga	ccgcatacaa	780
gatagggtga	ctggaaaata	tcaacggcaa	cttgctgcag	atcggacttc	cacgatttgg	840
gcgcgatttt	ataatctcga	agacaaccgc	ccattgtttg	gagatcgggg	caataacaatc	900
aaatacaact	ttgaggaggt	ttcagaggag	cgtagaaatg	gctatgcttg	gttcggcaac	960
tggccggaaa	agctgatcca	aaaggactat	ccaaaatgga	aaaaacaata	caaaattaaa	1020

taa

1023

<210> 50
 <211> 340
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(16)

<221> DOMAIN
 <222> (17)...(340)
 <223> Catalytic domain

<400> 50
 Met Leu Ser Phe Ile Ala Val Ser Val Phe His Asn Tyr Cys Thr Gly
 1 5 10 15
 Gln Thr Ala Ser Thr Lys Asn Ser Val Ala Glu Lys Met Leu Gln Tyr
 20 25 30
 Gln Leu Ser Asn Gly Ala Trp Pro Lys Gln Leu Val Asp Lys Ser Val
 35 40 45
 Val Asp Tyr Ser Leu Pro Leu Thr Lys Glu Arg Leu Gln Gln Ile Lys
 50 55 60
 Lys Thr Asp Ile Asp His Ala Thr Leu Asp Asn Ser Ala Thr Thr Arg
 65 70 75 80
 Glu Ile Thr Glu Leu Ile Lys Ala Phe Lys Asp Thr Lys Asn Lys Ala
 85 90 95
 Tyr Leu Thr Ala Val Glu Lys Gly Ile Ala Tyr Ile Leu Ser Ala Gln
 100 105 110
 Tyr Glu Asn Gly Gly Phe Pro Gln Tyr Tyr Pro Asn Lys Leu Tyr Tyr
 115 120 125
 Arg Ala Glu Ile Thr Tyr Asn Asp Asp Ala Met Ile Asn Ala Leu Leu
 130 135 140
 Val Leu Tyr Lys Val Ala Asn Lys Arg Glu Gly Phe Glu Ala Ile Asn
 145 150 155 160
 Pro Ile Phe Val Ser Lys Ala Gln Lys Ala Val Glu Lys Gly Ile Thr
 165 170 175
 Cys Ile Leu Lys Thr Gln Val Ile Gln Asp Gly Lys Arg Ser Ile Trp
 180 185 190
 Ala Ala Gln Tyr Asp Gln Asn Thr Leu Gln Pro Ala Gln Ala Arg Lys
 195 200 205
 Phe Glu Pro Ala Ser Leu Ser Thr Ser Glu Ser Val Ser Ile Val Arg
 210 215 220
 Phe Leu Met Leu Gln Pro Ala Thr Thr Glu Ile Lys Gln Ala Ile Glu
 225 230 235 240
 His Ala Ile Gln Trp Phe Glu Gln His Asp Ile Glu Gly Tyr Arg Phe
 245 250 255
 Asp Arg Ile Gln Asp Arg Val Thr Gly Lys Tyr Gln Arg Gln Leu Val
 260 265 270
 Ala Asp Arg Thr Ser Thr Ile Trp Ala Arg Phe Tyr Asn Leu Glu Asp
 275 280 285
 Asn Arg Pro Leu Phe Gly Asp Arg Asp Asn Thr Ile Lys Tyr Asn Phe
 290 295 300
 Glu Glu Val Ser Glu Glu Arg Arg Asn Gly Tyr Ala Trp Phe Gly Asn
 305 310 315 320
 Trp Pro Glu Lys Leu Ile Gln Lys Asp Tyr Pro Lys Trp Lys Lys Gln

Tyr Lys Ile Lys
340

325

330

335

<210> 51
<211> 1131
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 51
gtgacgtggg atcagatcct tcgtcagcct gccgcctggt acggcgggtcc ggaagcgcga 60
cggatcgaga atctggtcct gctgtaccag cgcgcgacgg ggggctggcc caagaacatc 120
gacatggcgc ggtcgtttgtc tccggacgat cgcacgacgc tcgcggcgga acggggccctc 180
accgactcga cgatcgacaa tggatcgacg acgacgcagt tgcggtttct cgcgatgggtg 240
cagcacgccc agcaggcacc cgtgcgcgac gccatcacgc acggcctgga ctatctgctg 300
aacgcgcaat actcgaacgg cggatggccg cagtactttc cgctccgaga cgactactcg 360
cgtcacatca cgttcaacga cgacgcgatg atcaatgtaa tgacgggtgct acgcgatgtc 420
gcagaagctc gcatgccctt cgaagggatc gacgcggtcc gtcgggaccg ggcgcggtgc 480
gccatcacgc gtggcatcga cgtgattctc gggacgcaaa tccgcgtcgg ggaccgtctg 540
acgggctggt gccagcagca tgacgagcgc tccctcgccc ccaccaaggc tcgcgcctac 600
gagcaccat cgatcgccag caaggaaacg gtaaccatca cgcgcttctc catgaccctc 660
gatcgccga gtcagcagat catcgcgcg cgtgagggcg atcgaggcgg ctgtcgagtg gttgcgcgtg 720
gcgaccctgt cgggtgtgcg agttgagcgt cggccggacc cggcgagtcc gaccggatat 780
gacgtcgtcg ccgcgccgga tgccgcgca cctccgacct gggcacgggt ctacgagatc 840
ggcagaacc gccaatggt ttccggccgc gacggcgtga tcagattccg gctcgcgagc 900
atcgagattg agcgcgcac cggctacagc tggatggcg actatgccgc gaggttgctg 960
aacgaggagt atccggcgtg ggcgaggcta cgccggcgga gctttcagaa cgccgagctg 1020
cacaaggagt ccggtgaagt cgtacacacg gcgatcgtgc acgatcttgc cttccttgat 1080
gtcgaagaca aagaccagcc gcagccgaaa gtgcttttcg ctgggcggta g 1131

<210> 52
<211> 376
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(376)
<223> Catalytic domain

<400> 52
Met Thr Trp Asp Gln Ile Leu Arg Gln Pro Ala Ala Trp Tyr Gly Gly
1 5 10 15
Pro Glu Ala Arg Ile Ala Asn Leu Val Leu Leu Tyr Gln Arg Ala
20 25 30
Thr Gly Gly Trp Pro Lys Asn Ile Asp Met Ala Arg Ser Leu Ser Pro
35 40 45
Asp Asp Arg Thr Thr Leu Ala Ala Glu Arg Ala Leu Thr Asp Ser Thr
50 55 60
Ile Asp Asn Gly Ser Thr Thr Thr Gln Leu Arg Phe Leu Ala Met Val
65 70 75 80
Gln His Ala Gln Gln Ala Pro Val Arg Asp Ala Ile Thr His Gly Leu
85 90 95
Asp Tyr Leu Leu Asn Ala Gln Tyr Ser Asn Gly Gly Trp Pro Gln Tyr

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Phe	Pro	Leu	Arg	Asp	Asp	Tyr	Ser	Arg	His	Ile	Thr	Phe	Asn	Asp	Asp
		115					120					125			
Ala	Met	Ile	Asn	Val	Met	Thr	Val	Leu	Arg	Asp	Val	Ala	Glu	Ala	Arg
		130				135					140				
Met	Pro	Phe	Glu	Gly	Ile	Asp	Ala	Val	Arg	Arg	Asp	Arg	Ala	Arg	Val
145					150					155					160
Ala	Ile	Thr	Arg	Gly	Ile	Asp	Val	Ile	Leu	Gly	Thr	Gln	Ile	Arg	Val
				165					170					175	
Gly	Asp	Arg	Leu	Thr	Gly	Trp	Cys	Gln	Gln	His	Asp	Glu	Arg	Ser	Leu
			180					185					190		
Ala	Pro	Thr	Lys	Ala	Arg	Ala	Tyr	Glu	His	Pro	Ser	Ile	Ala	Ser	Lys
		195					200					205			
Glu	Thr	Val	Thr	Ile	Thr	Arg	Phe	Leu	Met	Thr	Leu	Asp	Arg	Pro	Ser
	210					215					220				
Gln	Gln	Ile	Ile	Ala	Ala	Ile	Glu	Ala	Ala	Val	Glu	Trp	Leu	Arg	Val
225					230					235					240
Ala	Thr	Leu	Ser	Gly	Val	Arg	Val	Glu	Arg	Arg	Pro	Asp	Pro	Ala	Ser
				245					250					255	
Pro	Thr	Gly	Tyr	Asp	Val	Val	Ala	Ala	Pro	Asp	Ala	Ala	Ala	Pro	Pro
			260					265					270		
Thr	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Met	Phe	Ser
		275					280					285			
Gly	Arg	Asp	Gly	Val	Ile	Arg	Phe	Arg	Leu	Ala	Asp	Ile	Glu	Ile	Glu
	290					295					300				
Arg	Arg	Thr	Gly	Tyr	Ser	Trp	Met	Gly	Asp	Tyr	Ala	Ala	Arg	Leu	Leu
305					310					315					320
Asn	Glu	Glu	Tyr	Pro	Ala	Trp	Ala	Arg	Leu	Arg	Arg	Ala	Ser	Phe	Gln
				325					330					335	
Asn	Ala	Glu	Leu	His	Lys	Glu	Ser	Gly	Glu	Val	Val	His	Thr	Ala	Ile
			340					345					350		
Val	His	Asp	Leu	Ala	Phe	Leu	Asp	Val	Glu	Asp	Lys	Asp	Gln	Pro	Gln
		355					360					365			
Pro	Lys	Val	Leu	Phe	Ala	Gly	Arg								
	370					375									

<210>	53
<211>	1977
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	53						
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ctcgcaactg	caatcgcatc	accctcatgg	gcggcttgct	cttacagcgt	aaccaataat		120
tggggctctg	gctttaccgg	agaaattaaa	gtaaccaacg	atacaacatc	gactgtaaat		180
aattggtctg	tgtcttggca	ggaatcaggc	gtgaccgtca	ctaacgcgatg	gaatgcaca		240
ctgagcggat	caaatctcta	taccgcaaca	tcactcgggt	ggaacggaac	tctcgctcca		300
aaagcttcag	caagttttgg	ttttcaagca	aatggaacag	cgggcgcacc	gaaagtaa		360
ggaaccttgt	gtggtaccag	cacatcatca	acaggtacat	cctcagttgc	accttcatcc		420
gtagcgagta	gcgttgctgt	atcaagcagt	aaatcatcaa	gctctgttgc	aaccatcagt		480
agctctaaat	ccagcagcag	tgtgccgaca	gtttcatcat	tcactattca	ggaagagcaa		540
gccggtttct	gccgtgtaga	tggcattgca	actgaaagta	ctaacactgg	ctatacaggt		600
aatggctaca	ccaacaccac	taatgcgcaa	ggcgtgcgaa	ttgaatgggc	aatataatgc		660
cccaacagca	gccgtatac	ctcaccttc	cgttatgcca	atgctggatc	cgctaatacgc		720
aatggttcgt	tattataat	cgacgggaag	aatggtaact	acacagatgca	attgccaa		780
accggcgcat	gggcaacctg	gcaaacctgc	agtgttgaag	tggatttggt	gcaaggcaat		840

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aatattttga aactcgcttc gcttactgct gatggccttg cgaatataga ttcattaaaa 900
attgaaggcg cacaagccaa agctggtgta tgcagcacta cggtaagtag cagctcttcg 960
tcaattaaat caagttccag ttcattcatcg tccagctcaa ctgcagcagt aaaaacatta 1020
acactggatg gtaaccctgc tgcaaaactgg ttttaataaat ccagaaccaa gtggaatgtc 1080
agcagagctg acatcgctact ttcgtatcag caatcaaagt gtggctggcc aaaaaatttg 1140
gactacaact cggtaggctc aggtaatggt ggtagcgaca gcggcactat tgataatggt 1200
gcaaccataa ccgaaatggt gtacctcgct gaagtgtata aaaatggcgg gaataccaaa 1260
taccgcgacg ccgtgcgcag agcagcgaat tttattgtga gttcacaata cagcactggt 1320
gctttaccgc agttttatcc gctgaaaggt ggttacgcag atcacgctac ctttaatgat 1380
aatggtatgg cttacgcgctt gactgttctg gatttcgcgg taaataaacg cgcgccattt 1440
gataacgata ttttctctga ctctgaccgc agcaaattta aaactgctgt taccaaaggc 1500
gtcgattaca tattaanaagc gcaatggaaa cagaatggaa aattaaccgt atggtgcgca 1560
caacacggtg ctaatgatta tcaaccgaaa aaagcgcgtg cttacgagtt agaatacattg 1620
agtggtagtg aatctgtcgg tgtactcgct ttcttaatga ctcaaccaca aaccacgcaa 1680
attgaagcag ctgtgcgtgc aggtgtggcc tggtttaata gcccaagcac ctacttgaat 1740
aattacactt acgattcttc caaagcttcg accaatccaa tcgtgccaaa atccggaagc 1800
aaaatgtggt atcgctttta tgacctgaat accaaccgcg gtttcttcag tgatcgtgac 1860
ggcagcaagt tctacgacat cacccaaagt tcagaagagc gtcgcactgg ttacagttgg 1920
ggtggtgact acggcagctc gattatcagc ttcgcacaaa aagtgggata tctctaa 1977

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<210> 54

<211> 658

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(31)

<221> BINDING

<222> (32)...(124)

<223> Carbohydrate binding module

<221> BINDING

<222> (180)...(303)

<223> Carbohydrate binding module

<221> DOMAIN

<222> (304)...(658)

<223> Catalytic domain

<400> 54

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Met Asn Asn Ser Thr Lys Lys Met Ile Arg Pro Leu Lys Ala Ser Phe
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Ala Leu Gly Ala Leu Ala Leu Ala Ile Ala Ser Pro Ser Trp Ala Ala
 20           25           30
Cys Ser Tyr Ser Val Thr Asn Asn Trp Gly Ser Gly Phe Thr Gly Glu
 35           40           45
Ile Lys Val Thr Asn Asp Thr Thr Ser Thr Val Asn Asn Trp Ser Val
 50           55           60
Ser Trp Gln Glu Ser Gly Val Thr Val Thr Asn Ala Trp Asn Ala Thr
 65           70           75           80
Leu Ser Gly Ser Asn Pro Tyr Thr Ala Thr Ser Leu Gly Trp Asn Gly
 85           90           95
Thr Leu Ala Pro Lys Ala Ser Ala Ser Phe Gly Phe Gln Ala Asn Gly
100          105          110
Thr Ala Gly Ala Pro Lys Val Asn Gly Thr Leu Cys Gly Thr Ser Thr

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115	120	125
Ser Ser Thr Gly Thr Ser Ser	Val Ala Pro Ser Ser	Val Ala Ser Ser
130	135	140
Val Ala Val Ser Ser Ser	Lys Ser Ser Ser	Val Ala Thr Ile Ser
145	150	155
Ser Ser Lys Ser Ser Ser	Val Pro Thr Val Ser Ser	Phe Thr Ile
165	170	175
Gln Glu Glu Gln Ala Gly Phe	Cys Arg Val Asp Gly	Ile Ala Thr Glu
180	185	190
Ser Thr Asn Thr Gly Tyr Thr	Gly Asn Gly Tyr Thr	Asn Thr Thr Asn
195	200	205
Ala Gln Gly Ala Ala Ile	Glu Trp Ala Ile Asn	Ala Pro Asn Ser Ser
210	215	220
Arg Tyr Thr Leu Thr Phe	Arg Tyr Ala Asn Ala	Gly Thr Ala Asn Arg
225	230	235
Asn Gly Ser Leu Leu Ile	Asn Asp Gly Ser Asn	Gly Asn Tyr Thr Val
245	250	255
Gln Leu Pro Ser Thr Gly Ala	Trp Ala Thr Trp Gln	Thr Val Ser Val
260	265	270
Glu Val Asp Leu Val Gln Gly	Asn Asn Ile Leu Lys	Leu Ala Ser Leu
275	280	285
Thr Ala Asp Gly Leu Ala Asn	Ile Asp Ser Leu Lys	Ile Glu Gly Ala
290	295	300
Gln Ala Lys Ala Gly Val Cys	Ser Thr Thr Val Ser	Ser Ser Ser Ser
305	310	315
Ser Ile Lys Ser Ser Ser Ser	Ser Ser Ser Ser	Thr Ala Ala
325	330	335
Val Lys Thr Leu Thr Leu Asp	Gly Asn Pro Ala Ala	Asn Trp Phe Asn
340	345	350
Lys Ser Arg Thr Lys Trp Asn	Val Ser Arg Ala Asp	Ile Val Leu Ser
355	360	365
Tyr Gln Gln Ser Asn Gly Gly	Trp Pro Lys Asn Leu	Asp Tyr Asn Ser
370	375	380
Val Gly Ser Gly Asn Gly Gly	Ser Asp Ser Gly Thr	Ile Asp Asn Gly
385	390	395
Ala Thr Ile Thr Glu Met Val	Tyr Leu Ala Glu Val	Tyr Lys Asn Gly
405	410	415
Gly Asn Thr Lys Tyr Arg Asp	Ala Val Arg Arg Ala	Ala Asn Phe Ile
420	425	430
Val Ser Ser Gln Tyr Ser Thr	Gly Ala Leu Pro Gln	Phe Tyr Pro Leu
435	440	445
Lys Gly Gly Tyr Ala Asp His	Ala Thr Phe Asn Asp	Asn Gly Met Ala
450	455	460
Tyr Ala Leu Thr Val Leu Asp	Phe Ala Val Asn Lys	Arg Ala Pro Phe
465	470	475
Asp Asn Asp Ile Phe Ser Asp	Ser Asp Arg Ser Lys	Phe Lys Thr Ala
485	490	495
Val Thr Lys Gly Val Asp Tyr	Ile Leu Lys Ala Gln	Trp Lys Gln Asn
500	505	510
Gly Lys Leu Thr Val Trp Cys	Ala Gln His Gly Ala	Asn Asp Tyr Gln
515	520	525
Pro Lys Lys Ala Arg Ala Tyr	Glu Leu Glu Ser Leu	Ser Gly Ser Glu
530	535	540
Ser Val Gly Val Leu Ala Phe	Leu Met Thr Gln Pro	Gln Thr Thr Gln
545	550	555
Ile Glu Ala Ala Val Arg Ala	Gly Val Ala Trp Phe	Asn Ser Pro Ser
565	570	575
Thr Tyr Leu Asn Asn Tyr Thr	Tyr Asp Ser Ser Lys	Ala Ser Thr Asn
580	585	590

Pro Ile Val Pro Lys Ser Gly Ser Lys Met Trp Tyr Arg Phe Tyr Asp
 595 600 605
 Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg Asp Gly Ser Lys Phe
 610 615 620
 Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser Trp
 625 630 635 640
 Gly Gly Asp Tyr Gly Ser Ser Ile Ile Ser Phe Ala Gln Lys Val Gly
 645 650 655
 Tyr Leu

<210> 55
 <211> 1125
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 55
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 tggagcgcac gcctagtcca gcggcccga tggtagcggga gtgacgaagc gatccgcatc 180
 gcggacaacg tcctcctcta ccagcgcaac accggcgggt ggccgaagga catagatatg 240
 gccgagccca tcccgaaca caggaagtcc tttttcctca ccgagaagga gcggaccgat 300
 gactcgacca tcgacaacgg tgccaccgtg acccagctca agtatctcgc ccgcgtctac 360
 aaggcgacca ggctggaacg gttcaaggag ggcttcctca aagggtctcga ctacctcttg 420
 gccgcccagt acccgaacgg cggctggccc cagtattatc ctaacttgag gggctactac 480
 gccaacatca cttataacga caatgccatg gtgaacgtgc tcaccctcct ccagagcatc 540
 gccaaaaagg ccccgagta cgacttcgtc gaccggcgc gccgggagaa ggccgcccgg 600
 gccgtggcga aagggatcga ctgcatcctc aagaccaga tccgtgtcaa tggaaaactt 660
 accgcctggt gcgccagca tgaccccaag acgctggcgc ccgcgccggc ccgttcgtat 720
 gagcttgagt ccatcagcgg tttcgagagc gtcgggatcg tccggttctt aatgagcctc 780
 gagaatccga gcccggaagg catcgaggcg gtagaggccg ccgtgaaatg gttcgaggag 840
 gtcaagctta ccgggatcaa ggtggtcgag aaaccggacc cgtcccttcc gggcggttac 900
 gaccgcgtgg tggtcgaaga cccaacgcg ccgcccatct gggcccgggt ctacgagatc 960
 ggcaccaacc gtcccttctt ctgcggccgc gatggtatca aaaaatacag cctggcggag 1020
 atcgaacacg aacgccgggt cggttactcc tggtagacca atgcccggc ctacctcatc 1080
 gagaaggagt atccgctctg gcgggccaaa caccctacca agtaa 1125

<210> 56
 <211> 374
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(374)
 <223> Catalytic domain

<400> 56
 Met Val Leu Gly Asn Asn Gly Gly Ser Leu Ser Cys Val Gln Tyr Ile
 1 5 10 15
 Val Ile Val Lys Gly Pro Gly Gly Pro Arg Pro Pro Val Lys Pro Ala
 20 25 30
 Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Cys Leu Val Gln Arg
 35 40 45

Pro	Glu	Trp	Tyr	Gly	Ser	Asp	Glu	Ala	Ile	Arg	Ile	Ala	Asp	Asn	Val
50						55					60				
Leu	Leu	Tyr	Gln	Arg	Asn	Thr	Gly	Gly	Trp	Pro	Lys	Asp	Ile	Asp	Met
65					70					75					80
Ala	Glu	Pro	Ile	Pro	Glu	His	Arg	Lys	Ser	Phe	Phe	Leu	Thr	Glu	Lys
				85					90					95	
Glu	Arg	Thr	Asp	Asp	Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Val	Thr	Gln
			100					105					110		
Leu	Lys	Tyr	Leu	Ala	Arg	Val	Tyr	Lys	Ala	Thr	Arg	Leu	Glu	Arg	Phe
	115						120					125			
Lys	Glu	Gly	Phe	Leu	Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Ala	Ala	Gln	Tyr
	130					135						140			
Pro	Asn	Gly	Gly	Trp	Pro	Gln	Tyr	Tyr	Pro	Asn	Leu	Arg	Gly	Tyr	Tyr
145					150					155					160
Ala	Asn	Ile	Thr	Tyr	Asn	Asp	Asn	Ala	Met	Val	Asn	Val	Leu	Thr	Leu
			165						170					175	
Leu	Gln	Ser	Ile	Ala	Lys	Lys	Ala	Pro	Glu	Tyr	Asp	Phe	Val	Asp	Pro
		180					185						190		
Ala	Arg	Arg	Glu	Lys	Ala	Ala	Arg	Ala	Val	Ala	Lys	Gly	Ile	Asp	Cys
	195						200					205			
Ile	Leu	Lys	Thr	Gln	Ile	Arg	Val	Asn	Gly	Lys	Leu	Thr	Ala	Trp	Cys
	210					215						220			
Ala	Gln	His	Asp	Pro	Lys	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Arg	Ser	Tyr
225					230					235					240
Glu	Leu	Glu	Ser	Ile	Ser	Gly	Phe	Glu	Ser	Val	Gly	Ile	Val	Arg	Phe
			245						250					255	
Leu	Met	Ser	Leu	Glu	Asn	Pro	Ser	Pro	Lys	Val	Ile	Glu	Ala	Val	Glu
		260						265					270		
Ala	Ala	Val	Lys	Trp	Phe	Glu	Glu	Val	Lys	Leu	Thr	Gly	Ile	Lys	Val
	275						280					285			
Val	Glu	Lys	Pro	Asp	Pro	Ser	Leu	Pro	Gly	Gly	Tyr	Asp	Arg	Val	Val
	290					295					300				
Val	Glu	Asp	Pro	Asn	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr	Glu	Ile
305					310					315					320
Gly	Thr	Asn	Arg	Pro	Phe	Phe	Cys	Gly	Arg	Asp	Gly	Ile	Lys	Lys	Tyr
			325						330					335	
Ser	Leu	Ala	Glu	Ile	Glu	His	Glu	Arg	Arg	Val	Gly	Tyr	Ser	Trp	Tyr
		340					345						350		
Thr	Asn	Ala	Pro	Ala	Tyr	Leu	Ile	Glu	Lys	Glu	Tyr	Pro	Leu	Trp	Arg
	355						360						365		
Ala	Lys	His	Pro	Thr	Lys										
	370														

<210> 57

<211> 1170

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 57

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cccgaaaatt	tcctcaaagg	caaagacggc	tggaatccga	aaaaggcgga	tgaccgctgg	120
ctcgaaaaaa	caaaacctga	ctggcagctc	gttacgtgga	acgacgcgtt	acgccaggcg	180
ccgctctggt	atcaaaccga	tgaagcggcg	cgcattgccg	accaggtgat	tttgtaccag	240
aaagacaacg	gcggctggga	aaaaaatctc	gatatgacgg	cgatgctcac	gcaagccgaa	300
cgcgaaaagc	tcgccaaaaga	aaaatcgaac	acgtcggaac	cgacgatcga	caaccgcacg	360
acctacacgc	aagtcgcttt	tctcgccaaa	gtcattacgg	gcagcttgca	gaaaacgact	420

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ccgccgacca atttcccgaa acataaggaa gcttttttca agggccttga ttacctgctc 480
gcgtcgcagt acgaatcggg cggcttttccg cagtttttacc cgctcaaaaa aggttattac 540
acgcacatca cgttcaacga cgatgcgatg attggcggtt tgaagggttt gcgcgaaatc 600
gccaaaaaga aggaagacta tctttttgtt gacgaagaac gccgcctgaa agcggaaaaa 660
tcggtcgaaa aagcgctgcc gctgattctg aaattgcagg ttgaagtcgg cggcaaaaaa 720
acggttttgg cggcgcagta tgacgaaaac acttttaaac ccgcagcggc gcgaaagtgt 780
gaaccgggtt ctttaacggc gggcgaaatc gtcggcatcg tccggttttt aatgtacgat 840
tcaaagcccg accagcgac gattgacgag attgaatctg ccattcagtg gtatcgcgcg 900
aacaaaatcg aaggcattcg atgggtgcgc gaaaacggcg aaaaccgcgt cgtcaaggac 960
aaaaacgcgc cgccgatttg ggcgcgggtt tacgaaatcg aaacgatgaa gccgattttc 1020
atcgggcgcg acgccatcat tcgttacgac gtgtctgaaa tcgaagccga gcgccgcaac 1080
ggctacgcgt ggtacgtctc ggagccgaac gagctgcttg aaaaagatta cccgaaatgg 1140
ctggaaaaaa ttaaaaaatc agtaaagtaa 1170

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<210> 58
 <211> 389
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(389)
 <223> Catalytic domain

<400> 58

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Lys	Gln	Phe	Glu	Pro	Glu	Asn	Phe	Leu	Lys	Gly	Lys	Asp	Gly	Trp	Asn	20	25	30	
Pro	Lys	Lys	Ala	Asp	Asp	Arg	Trp	Leu	Glu	Lys	Thr	Lys	Pro	Asp	Trp	35	40	45	
Gln	Leu	Val	Thr	Trp	Asn	Asp	Ala	Leu	Arg	Gln	Ala	Pro	Leu	Trp	Tyr	50	55	60	
Gln	Thr	Asp	Glu	Ala	Ala	Arg	Ile	Ala	Asp	Gln	Val	Ile	Leu	Tyr	Gln	65	70	75	80
Lys	Asp	Asn	Gly	Gly	Trp	Glu	Lys	Asn	Leu	Asp	Met	Thr	Ala	Met	Leu	85	90	95	
Thr	Gln	Ala	Glu	Arg	Glu	Lys	Leu	Ala	Lys	Glu	Lys	Ser	Asn	Thr	Ser	100	105	110	
Glu	Thr	Thr	Ile	Asp	Asn	Arg	Thr	Tyr	Thr	Gln	Val	Ala	Phe	Leu		115	120	125	
Ala	Lys	Val	Ile	Thr	Gly	Ser	Leu	Gln	Lys	Thr	Thr	Pro	Pro	Thr	Asn	130	135	140	
Phe	Pro	Lys	His	Lys	Glu	Ala	Phe	Phe	Lys	Gly	Leu	Asp	Tyr	Leu	Leu	145	150	155	160
Ala	Ser	Gln	Tyr	Glu	Ser	Gly	Gly	Phe	Pro	Gln	Phe	Tyr	Pro	Leu	Lys	165	170	175	
Lys	Gly	Tyr	Tyr	Thr	His	Ile	Thr	Phe	Asn	Asp	Asp	Ala	Met	Ile	Gly	180	185	190	
Val	Leu	Lys	Val	Leu	Arg	Glu	Ile	Ala	Lys	Lys	Lys	Glu	Asp	Tyr	Leu	195	200	205	
Phe	Val	Asp	Glu	Glu	Arg	Arg	Leu	Lys	Ala	Glu	Lys	Ser	Val	Glu	Lys	210	215	220	
Ala	Leu	Pro	Leu	Ile	Leu	Lys	Leu	Gln	Val	Glu	Val	Gly	Gly	Lys	Lys	225	230	235	240
Thr	Val	Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Asn	Thr	Phe	Lys	Pro	Ala	Ala	245	250	255	

Ala	Arg	Lys	Phe	Glu	Pro	Val	Ser	Leu	Thr	Ala	Gly	Glu	Ser	Val	Gly
			260					265					270		
Ile	Val	Arg	Phe	Leu	Met	Tyr	Asp	Ser	Lys	Pro	Asp	Gln	Ala	Thr	Ile
		275					280					285			
Asp	Ala	Ile	Glu	Ser	Ala	Ile	Gln	Trp	Tyr	Arg	Ala	Asn	Lys	Ile	Glu
		290				295					300				
Gly	Ile	Arg	Trp	Val	Arg	Glu	Asn	Gly	Glu	Asn	Arg	Val	Val	Lys	Asp
		305			310				315						320
Lys	Asn	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Glu	Thr	Met
			325					330						335	
Lys	Pro	Ile	Phe	Ile	Gly	Arg	Asp	Ala	Ile	Ile	Arg	Tyr	Asp	Val	Ser
			340					345					350		
Glu	Ile	Glu	Ala	Glu	Arg	Arg	Asn	Gly	Tyr	Ala	Trp	Tyr	Val	Ser	Glu
		355					360					365			
Pro	Asn	Glu	Leu	Leu	Glu	Lys	Asp	Tyr	Pro	Lys	Trp	Leu	Glu	Lys	Ile
	370					375					380				
Lys	Lys	Ser	Val	Lys											
															385

<210> 59
 <211> 1080
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 59	
atgagaatcc ggtcctcttc aatcgcgttc ggcctgattt gcagtctggc gctaaggggtg	60
cctgcgcaag cgcaggtcac cgtgcgctgg gcgacgtcc tgaaccagcc cgccgcctgg	120
tatggcaccg atgaagcccg tcgaattgcc gaccacgtgc tcgagcatca acgagcggaa	180
ggcggatggc caaagaacac ggacatgacc gcagcgcccg atccggcggt gctcacagcc	240
gcgcgagtga agccagactc gacgatcgat aacggcgcgga ccgtcactga aatgcgcgtc	300
ctcgcgcgcg tctaccgttc atcacccgat ccccgttatc gcgatgcgct gctcaagggt	360
ctcgactatc tgttggcagc gcagtatgcc aacggcggtt ggccgcagtt ctaccgcgtc	420
cggcaggact attcgcgcta tatcacgttc aacgacaacg cgatgatcaa tgtcgtgacg	480
ctgctctcag acgtcgctgc cggaaatggc gactgggcgt ttgctgatgc cagccggcgc	540
gagaaaagcc ggacggctgt agagaaggcc gtagaagtca tcctgcgcgc gcaggtgaga	600
gttgacggcc ggctgacgc gtggtgcgcc caacacgacg aggtgacact cgagccgcgc	660
aaggcccgcg cctacgaaca tccgtcgctg agcggacagg agacgggtggg gatcatccgg	720
tttctcatga cccgcgataa accggatcag agagtcgtcg atgcaatcga ggcgtcagtg	780
gcatggctga aggcggtgca gctcaaagga cttcgcgtcg accagcgccg cgatccctcg	840
ctgccggagg ggcgtgacgt ggtgaccgtc gctgaccggt cggcgccgcc gctctgggcg	900
cgcttctacg aaatcgggac caatcgcgcc atcttctctg gacgcgacgg cgtgatccga	960
tactcgctgg cagagatcga gcacgaacgc cggatagggt acgcctggct cggaacctgg	1020
cccgcgaagc tgctcgatac cgaataccca tcctggcgac ggactcaaca aaggccgtga	1080

<210> 60
 <211> 359
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(24)

<221> DOMAIN

<222> (25)...(359)

<223> Catalytic domain

<400> 60

```

Met Arg Ile Arg Ser Ser Ser Ile Ala Phe Gly Leu Ile Cys Ser Leu
 1          5          10
Ala Leu Arg Val Pro Ala Gln Ala Gln Val Thr Val Arg Trp Ala Asp
          20          25          30
Val Leu Asn Gln Pro Ala Ala Trp Tyr Gly Thr Asp Glu Ala Arg Arg
          35          40          45
Ile Ala Asp His Val Leu Glu His Gln Arg Ala Glu Gly Gly Trp Pro
          50          55          60
Lys Asn Thr Asp Met Thr Ala Ala Pro Asp Pro Ala Val Leu Thr Ala
65          70          75          80
Ala Arg Val Lys Pro Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr
          85          90          95
Glu Met Arg Val Leu Ala Arg Val Tyr Arg Ser Ser Pro Asp Pro Arg
          100          105          110
Tyr Arg Asp Ala Leu Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln
          115          120          125
Tyr Ala Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu Arg Gln Asp Tyr
          130          135          140
Ser Arg Tyr Ile Thr Phe Asn Asp Asn Ala Met Ile Asn Val Val Thr
145          150          155          160
Leu Leu Ser Asp Val Ala Ala Gly Asn Gly Asp Trp Ala Phe Ala Asp
          165          170          175
Ala Ser Arg Arg Glu Lys Ser Arg Thr Ala Val Glu Lys Ala Val Glu
          180          185          190
Val Ile Leu Arg Ala Gln Val Arg Val Asp Gly Arg Leu Thr Ala Trp
          195          200          205
Cys Ala Gln His Asp Glu Val Thr Leu Glu Pro Arg Lys Ala Arg Ala
210          215          220
Tyr Glu His Pro Ser Leu Ser Gly Gln Glu Thr Val Gly Ile Ile Arg
225          230          235          240
Phe Leu Met Thr Arg Asp Lys Pro Asp Gln Arg Val Val Asp Ala Ile
          245          250          255
Glu Ala Ser Val Ala Trp Leu Lys Ala Val Gln Leu Lys Gly Leu Arg
          260          265          270
Val Asp Gln Arg Arg Asp Pro Ser Leu Pro Glu Gly Arg Asp Val Val
          275          280          285
Thr Val Ala Asp Pro Ser Ala Pro Pro Leu Trp Ala Arg Phe Tyr Glu
          290          295          300
Ile Gly Thr Asn Arg Pro Ile Phe Ser Gly Arg Asp Gly Val Ile Arg
305          310          315          320
Tyr Ser Leu Ala Glu Ile Glu His Glu Arg Arg Ile Gly Tyr Ala Trp
          325          330          335
Leu Gly Thr Trp Pro Ala Lys Leu Leu Asp Thr Glu Tyr Pro Ser Trp
          340          345          350
Arg Arg Thr Gln Gln Arg Pro
          355

```

<210> 61

<211> 1224

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

```

<400> 61
gtggaattac cagtaaccgg cgcattgggca acctggcaaa ccgcaactgt tgaaattgat      60
tttgtgcaag gtaacaacct gttaaaactt tctgcgatca cggctgatgg ttgggcaaat      120
atcgattcgt tgaaaattga cggcgacaaa accaaagccg gcgtgtgcag cactgtggca      180
agcagcagct cttcatccgt tgcttcatcg attaaatcaa gctccagttc atcctcttcc      240
agttcaacga cgacggtaaa aacattaaca ctggatggca accccgcagc aaactggttt      300
aacaaatcca gaaccaaatg gaataaccagc agagccgatg ttgtactttc ctatcaacaa      360
tccaacggcg gctggccaaa aaatctcgat tacaattcag taagcgcagg taatggcggc      420
agcgatagcg gcaccatcga taacggtgca accattactg aaatgggtta tctcgcggaa      480
gtttacaaaa atggcaacaa caccaagtat cgcgatgagg tgcgagagc cgcaaatttt      540
attgtcagct cgcaatacag cactggtgca ttaccacaat tttatccatt gaaaggcggc      600
tatgcagacc acgccacctt taacgataac ggcattggat atgcattaac ggtattggat      660
tttgagtcga acaaacgcgc cccatttgat actgatgttt tctccgattc tgatcgcgcg      720
aaattcaaaa ccgctgttgc caaagggtgtg gattacattt tgaaagcgca gtggaaacaa      780
aacggaaaat taaccgtgtg gtgtgcacaa catggtgcta ccgattatca accgaaaaaa      840
gcgcgcgcct atgaattgga atcactgagt ggcagcgaat ctggtgggtg actcgttttc      900
ttgatgaccc aaccgcaaac cgcacaaatt gaagccgctg taaaagccgg tgtagcctgg      960
ttcaatagcc ccaacacgta tttgaacaat tacacttacg actcttcaaa agcgtcaact     1020
aatccaatag ttgccaagtc tggaagcaaa atgtggtatc gcttttacga tttaaatacc     1080
aatcggtggc tcttcagtga tcgcgatggc agcaaattct atgacatcac ccagatgtca     1140
gaagagcgtc gcactggata tagctggggg ggtgattacg gcacgtcgat tatttccttc     1200
gcgcaaaaag tgggatattc gtaa                                     1224

```

```

<210> 62
<211> 407
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample

```

```

<221> DOMAIN
<222> (0)...(407)
<223> Catalytic domain

```

```

<400> 62
Met Glu Leu Pro Val Thr Gly Ala Trp Ala Thr Trp Gln Thr Ala Thr
1      5      10      15
Val Glu Ile Asp Leu Val Gln Gly Asn Leu Leu Lys Leu Ser Ala
20     25     30
Ile Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys Ile Asp Gly
35     40     45
Ala Gln Thr Lys Ala Gly Val Cys Ser Thr Val Ala Ser Ser Ser Ser
50     55     60
Ser Ser Val Ala Ser Ser Ile Lys Ser Ser Ser Ser Ser Ser Ser
65     70     75     80
Ser Ser Thr Thr Thr Val Lys Thr Leu Thr Leu Asp Gly Asn Pro Ala
85     90     95
Ala Asn Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Thr Ser Arg Ala
100    105    110
Asp Val Val Leu Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn
115    120    125
Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly
130    135    140
Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu
145    150    155    160
Val Tyr Lys Asn Gly Asn Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg
165    170    175
Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro

```

```

<210> 63
<211> 1023
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 63
atgttaagtt tcatcgcggt atcagtggtt cataattact gtacagggca gactgcgctcc
acaaaaaatt cagtggccga aaagatgctt cagtaccagt tgtcaaatgg cgcctggccc
aaacagtttg tagacaaaag tgtcgttgat tacagtcttc cattaacgaa agagctccta
cagcagatca agaaaacaga tattgatcat gctacgctcg acaacagtg cacaaccgga
gaaataactg aattgatcaa ggcttttaag gacactaaaa ataaggcata tttgactgct
gcagaaaagg ggattgcata tttttatcgc gctcaatatg agaatggcgg atttccacaa
tactacccaa ataaattata ctatagagct gagataacat acaacgatga tgcgatgatc
aatgcattac tagtgcttta caaagtagcc aataaagcgag aggggtttga ggctatcaat
cccatatttg tgtcaaaagc gcaaaaagca gttgaaaagg gtataacctg tatcctaaaa
acacagggtc tacaagacgg aaaaaggagt atttgggctg cgcaatacga tcagaacact
ttacaacctg ctcaggcaag aaagtttgaa ccagcttcat tgagcacaag tgaatctgtt
tccatcgctt gctttctcat gctacagcct gcaaccactg aaattaagca agcgatcgaa
catgcaatac aatgggttcga acagcatgat attgaagggt accggttcga ccgcatacaa
gatagggtga ctggaaaata tcaacggcag cttgtcgctg atcggacttc cacgatttgg
gcgcgatttt ataatctcga agacaaccgt ccattgtttg gagatcggga caataacaatc
aaatacaact ttgaggagggt ttcagaggag cgtagaaatg gctatgcttg gttcggcaac
tggccggaaa agctgatcca aaaggactat ccaaaatgga aaaaacaata caaaattcaa
taa

```

<210> 64

<211>	340
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

```
<221> SIGNAL
<222> (1) ... (16)
```

```
<221> DOMAIN
<222> (17)...(340)
<223> Catalytic domain
```

<400> 64

[illegible]

<210> 65
 <211> 1311
 <212> DNA
 <213> Bacteria

<400> 65
 gtgaaccgac gtacccgcct gggagcgggc gccgcgaccg ccctcgccct gacggtcacc 60
 gccccgcgcg ccggtgcca cgccgcgcgt cccacgcgcg cgccacgccc ggtcgccgat 120
 ccggctcgcg ccacgctgcc cgccggcgac ggctgggcgt ccgaggggac cggcacgacc 180
 ggtgggggcg ccgccgaggc ctcccgggtc ttaccgctcg ccacctggga ggagttccgg 240
 gccgcgctcg cgggtgcccg ctccgagccc aggatcgta aggtgggtgg cacgctgaac 300
 gccaccgcgc cgggtgcgcg cgccttcgag gcgcgggcgt acgacttcgc ccgctacctc 360
 gccgactacg acccgccggt gtgggggtac gagaaggagg tcagcgggcc gcaggaggag 420
 ctgcggggcg cgtccgcgac cgcgcagggc caggccatca aggtcaaggt gccggcgaac 480
 accacgatcg tcggggtcgg caggcacgcg gggatcacgc gcggcagcct ccaggtgcag 540
 ggcgtcgaca acgtcggtgt ccgcaacctg acgctggaga gccgctcga ctgcttcccg 600
 cagtgggacc cgaccgacgg cgcgaccggg gcgtggaact ccgagtacga cagcctcgtc 660
 gtgtacggct ccacccatgt ctggatcgac cacaacacct tcaccgacgg cgcccaccg 720
 gacagttcgc tgccctcgta ctacggcgag gtctaccagc agcacgacgg cgaactggac 780
 gtcgtgcggg gcgcggacct cgtcacggtc tgcgtggaacg ccttcaccga ccacgacaag 840
 accctgatga tcggcaacag cgacagcgcg ggcgccaccg accggggcaa gctgcgggtc 900
 accctgcacc acaacctgtt cgagaacgtc gtcgagcggg cgccccgggt caggttcggg 960
 caggtcgacg cgtacaacaa ccacttcgtc gtgccgagtt cggcctacgc gtacagcctg 1020
 ggcgtcgggc aggagtcca gctcttcgcg gagaagaacg cgttcaccct cgccgggggc 1080
 gtgccggccg ggaagatcct caagaagtgg aaggacgcgc ccgtcaccac cgtcggcaac 1140
 tacgtgaacg gcaggccggt cgacctgctc gccgtccaca acaccagtt cccggaggag 1200
 cagttgcggg ccgacgcggg ctggaccccc gtcctgcgca ccagggtcga ccaccgagg 1260
 gccgtccccg cgctcgtcga ccaccgcgcg ggcgcgggcc gtcctgctg a 1311

<210> 66
 <211> 436
 <212> PRT
 <213> Bacteria

<220>

<221> SIGNAL
 <222> (1)...(28)

<221> DOMAIN
 <222> (29)...(436)
 <223> Catalytic domain

<400> 66
 Met Asn Arg Arg Thr Arg Leu Gly Ala Val Ala Ala Thr Ala Leu Ala
 1 5 10 15
 Leu Thr Val Thr Ala Pro Ala Ala Gly Ala His Ala Ala Ala Pro His
 20 25 30
 Ala Ala Pro Arg Pro Val Ala Asp Pro Ala Arg Ala Thr Leu Pro Ala
 35 40 45
 Gly Asp Gly Trp Ala Ser Glu Gly Thr Gly Thr Thr Gly Gly Ala Ala
 50 55 60
 Ala Glu Ala Ser Arg Val Phe Thr Val Ala Thr Trp Glu Glu Phe Arg
 65 70 75 80
 Ala Ala Leu Ala Val Pro Gly Ser Glu Pro Arg Ile Val Lys Val Val
 85 90 95
 Gly Thr Leu Asn Ala Thr Ala Ala Gly Cys Gly Ala Phe Glu Ala Pro
 100 105 110

Gly Tyr Asp Phe Ala Arg Tyr Leu Ala Asp Tyr Asp Pro Ala Val Trp
115 120 125
Gly Tyr Glu Lys Glu Val Ser Gly Pro Gln Glu Glu Leu Arg Ala Ala
130 135 140
Ser Ala Thr Ala Gln Gly Gln Ala Ile Lys Val Lys Val Pro Ala Asn
145 150 155 160
Thr Thr Ile Val Gly Val Gly Arg His Ala Gly Ile Thr Gly Gly Ser
165 170 175
Leu Gln Val Gln Gly Val Asp Asn Val Val Val Arg Asn Leu Thr Leu
180 185 190
Glu Ser Pro Leu Asp Cys Phe Pro Gln Trp Asp Pro Thr Asp Gly Ala
195 200 205
Thr Gly Ala Trp Asn Ser Glu Tyr Asp Ser Leu Val Val Tyr Gly Ser
210 215 220
Thr His Val Trp Ile Asp His Asn Thr Phe Thr Asp Gly Ala His Pro
225 230 235 240
Asp Ser Ser Leu Pro Ser Tyr Tyr Gly Glu Val Tyr Gln Gln His Asp
245 250 255
Gly Glu Leu Asp Val Val Arg Gly Ala Asp Leu Val Thr Val Ser Trp
260 265 270
Asn Ala Phe Thr Asp His Asp Lys Thr Leu Met Ile Gly Asn Ser Asp
275 280 285
Ser Ala Gly Ala Thr Asp Arg Gly Lys Leu Arg Val Thr Leu His His
290 295 300
Asn Leu Phe Glu Asn Val Val Glu Arg Ala Pro Arg Val Arg Phe Gly
305 310 315 320
Gln Val Asp Ala Tyr Asn Asn His Phe Val Val Pro Ser Ser Ala Tyr
325 330 335
Ala Tyr Ser Leu Gly Val Gly Gln Glu Ser Gln Leu Phe Ala Glu Lys
340 345 350
Asn Ala Phe Thr Leu Ala Gly Gly Val Pro Ala Gly Lys Ile Leu Lys
355 360 365
Lys Trp Lys Asp Ala Pro Val Thr Thr Val Gly Asn Tyr Val Asn Gly
370 375 380
Arg Pro Val Asp Leu Leu Ala Val His Asn Thr Gln Phe Pro Glu Glu
385 390 395 400
Gln Leu Arg Ala Asp Ala Gly Trp Thr Pro Val Leu Arg Thr Arg Val
405 410 415
Asp His Pro Arg Ala Val Pro Ala Leu Val Asp His Arg Ala Gly Ala
420 425 430
Gly Arg Ser Cys
435

<210> 67

<211> 1995

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 67

atgaaaaatt	caaaaactgt	ttttactgca	caaaaaaac	tcatgcactc	ttgcattgcc	60
gccgctatcg	gcttggcgat	aagttcaggt	gcttggtcag	cttgtactta	cactgtcacc	120
aataattggg	gttctggctt	caccggtgaa	atcaaagtta	ccaacaacac	atcatcggct	180
gtaaatgggt	ggtctgtgtc	ttggcaggaa	tcaggcgcat	cagtcaccaa	ctcatggaac	240
gcaactctga	gcggtatcaa	tccttatacg	gcagccgcct	taggttggaa	tgcaactctc	300
gcacccggtg	cttctgccag	ttttggcttt	caagcaaattg	gcactgctag	cgcacctaaa	360
gtgaatggca	ctttatgtgg	aacagctact	tcatcaaacac	ctgcgtcatc	cagcagtggt	420

```

gcgagttcgg ttaaatcaag cgcacccggt tcgtccagca gtaaatcatc cagctcaatc 480
actgtgagta gtagttctat cgccagcagc agcgcaccaa gtgtttcttc attaacaatt 540
caggaagagc aagctggcgt ctgtcgtggt gatggcattg caacagaaag caccaacacc 600
ggctttaccg gcaacggcta taccaatgca aacaacgcac aaggtgcagc gattgaatgg 660
gcggtaaatg caccgagcag tggccgctac acactcacat tccgttttgc aaatggcggc 720
actgcagcac gcaatgggtc actgttaatt aacggcggta gcaatggtaa ctacaccgtg 780
gatttaccac taaccggcgc atgggcgact tggcaaacag cgactgtaga aatcgatttg 840
gtacaaggca ccaacacgct gaaactttct gcattaaccg cagatggctt agctaatatc 900
gattcattaa aaattgatgg caaccaaccg aaagcaggca cttgcagcaa tacatcaagc 960
agtgttgcca gcagttcttc atccgttaaa tccagttcaa gttcttcac aagctcatcc 1020
accactgcaa aaatgctgac tcttgatggc aaccccgccg caagttgggt caacaaatcc 1080
agaaccaaat ggaatagcag tcgtgcggac attgtgttgt cttaccagca agctaaccggc 1140
ggctggccaa aaaatctgga ttacaactca gtaagcgcag gtaatgggtg tagcgacagc 1200
ggcactatcg acaacggcgc aaccatcacg gaaatgggtt atctcgaga agtttataaa 1260
aacgggggca atacaaaata tcgcgatgca gtacgtaaag cggcaaactt tattgtgagt 1320
tcgcaataca gcaactggtc gttaccacaa ttttaccat tgaaagggtg ttatgcagat 1380
cacgccacct ttaacgataa cggcatggct tacgcattaa cggtattgga ttttgcggtg 1440
aacaaacgtg cgccgtttga taacgatgta ttttctgat cagaccgcgc aaaattcaaa 1500
actgccgtga ccaaaggat tgattacatt ttgaaagccc aatggaaaaca aaatggaaaa 1560
ctcaccgcat ggtgtgcgca acacggagca aacgactatc aacaaaaagc ggcgcggtgct 1620
tatgagttag tatctttaag cggcagcgaa tccgttggca tcatcgcttt cctgatgacc 1680
caaccacaaa ctgcgcaaat cgaagcagcg gttaaagccg gtgtaaaactg gttcgctagc 1740
ccgaatacat acttggttaa ttacacctac gactcgtcaa aagcctctac caatccgatt 1800
gtgtacaaat ccggcagcag aatgtggtat cgcttctacg atctgaacac caatcgcgga 1860
ttcttttagtg atcgcgatgg cagcaaatc tatgacatca ctcaaatgtc tgaagaacgt 1920
cgcaccggct acagctgggg cggttcttac ggtgaatcga ttatcagctt cgcgcaaaaa 1980
gtgggttatc tctaa

```

<210> 68
 <211> 664
 <212> PRT
 <213> Unknown

<220> .
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(32)

<221> BINDING
 <222> (33)...(126)
 <223> Carbohydrate binding module

<221> BINDING
 <222> (184)...(307)
 <223> Carbohydrate binding module

<221> DOMAIN
 <222> (308)...(664)
 <223> Catalytic domain

```

<400> 68
Met Lys Asn Ser Lys Thr Val Phe Thr Ala Gln Lys Lys Leu Met His
 1           5           10           15
Ser Cys Ile Ala Ala Ile Gly Leu Ala Ile Ser Ser Gly Ala Trp
          20           25           30
Ser Ala Cys Thr Tyr Thr Val Thr Asn Asn Trp Gly Ser Gly Phe Thr
          35           40           45
Gly Glu Ile Lys Val Thr Asn Asn Thr Ser Ser Ala Val Asn Gly Trp

```

50	55	60
Ser Val Ser Trp Gln Glu Ser Gly Ala Ser Val Thr Asn Ser Trp Asn		
65	70	75
Ala Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Ala Ala Leu Gly Trp		80
	85	90
Asn Ala Thr Leu Ala Pro Gly Ala Ser Ala Ser Phe Gly Phe Gln Ala		95
	100	105
Asn Gly Thr Ala Ser Ala Pro Lys Val Asn Gly Thr Leu Cys Gly Thr		110
	115	120
Ala Thr Ser Ser Thr Pro Ala Ser Ser Ser Ser Val Ala Ser Ser Val		125
	130	135
Lys Ser Ser Ala Pro Val Ser Ser Ser Ser Lys Ser Ser Ser Ser Ile		140
145	150	155
Thr Val Ser Ser Ser Ser Ile Ala Ser Ser Ser Ala Pro Ser Val Ser		160
	165	170
Ser Leu Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly		175
	180	185
Ile Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr		190
	195	200
Asn Ala Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Asn Ala		205
	210	215
Pro Ser Ser Gly Arg Tyr Thr Leu Thr Phe Arg Phe Ala Asn Gly Gly		220
225	230	235
Thr Ala Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly		240
	245	250
Asn Tyr Thr Val Asp Leu Pro Leu Thr Gly Ala Trp Ala Thr Trp Gln		255
	260	265
Thr Ala Thr Val Glu Ile Asp Leu Val Gln Gly Thr Asn Thr Leu Lys		270
	275	280
Leu Ser Ala Leu Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys		285
	290	295
Ile Asp Gly Asn Gln Pro Lys Ala Gly Thr Cys Ser Asn Thr Ser Ser		300
305	310	315
Ser Val Ala Ser Ser Ser Ser Val Lys Ser Ser Ser Ser Ser Ser		320
	325	330
Ser Ser Ser Ser Thr Thr Ala Lys Met Leu Thr Leu Asp Gly Asn Pro		335
	340	345
Ala Ala Ser Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg		350
	355	360
Ala Asp Ile Val Leu Ser Tyr Gln Gln Ala Asn Gly Gly Trp Pro Lys		365
	370	375
Asn Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser		380
385	390	395
Gly Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala		400
	405	410
Glu Val Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg		415
	420	425
Lys Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu		430
	435	440
Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe		445
	450	455
Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val		460
465	470	475
Asn Lys Arg Ala Pro Phe Asp Asn Asp Val Phe Ser Asp Ala Asp Arg		480
	485	490
Ala Lys Phe Lys Thr Ala Val Thr Lys Gly Ile Asp Tyr Ile Leu Lys		495
	500	505
Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His		510
	515	520
		525

Gly Ala Asn Asp Tyr Gln Pro Lys Ala Ala Arg Ala Tyr Glu Leu Val
 530 535 540
 Ser Leu Ser Ser Gly Ser Glu Ser Val Gly Ile Ile Ala Phe Leu Met Thr
 545 550 555 560
 Gln Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn
 565 570 575
 Trp Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser
 580 585 590
 Ser Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met
 595 600 605
 Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp
 610 615 620
 Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg
 625 630 635 640
 Arg Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser
 645 650 655
 Phe Ala Gln Lys Val Gly Tyr Leu
 660

<210> 69
 <211> 1035
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 69
 atggcgcggtt tgttccgggtg cgtgtgtgtgcc agcctgggag gatggggccgc ggttctggcc 60
 gccgcggcgcg gcccggtattg gtccgcctg ctgcgcgaac cggacccttg gtttcgcagt 120
 ccggcgggggc aacaggcggt gacgaacgtt ttgtcctggc agagcgcgac aggcgccttg 180
 ccgaaaaacc tggacaccac ccgcgagccg cgtcggcagg attccgcccc gcccgaggcg 240
 actttcgaca acggcgccac caccggcgag ttgcggtttc tggcgcgggc gtttgcggcc 300
 accggcgatc cgcgctgcga agccgcgggtg ctccgggggc tggacggcat cctcgcggcc 360
 cagcttccca gcggcggtg gccgcagtgt catcctccgc gcgcgcctta tcagcgccac 420
 atcaccttca acgacgggtgt catggtgcgc atcctggagc tgctgcgcga gatagaccgc 480
 gcgcgggagt ttcgctgggt ggacgaggcg cggcgcgcg gcggtgcgcgc ggccttcaact 540
 cgcggggctgg agtgccctct gcgctgccag gtggtcgtcg agggcagact caccgtgtgg 600
 tgtgcccagc atgacgcgga gaactttcaa ccgcgaccgg cacgcgccta cgaactggaa 660
 tcgctcagcg gcgcggaaaag cgcgggcac ctggtgttcc tcatgagcct ggagccgcca 720
 acccgcgaga tcgcgcgcgc ggtcgaggcc gggcgggcct ggttttcggc ggtaaagctt 780
 gaagggttcc gtctcgaacg aacggccgac gacgcgcggg tgggtggaaga gccgggcgcg 840
 ccgcgcgtct gggcgcggtt ctacgagatc gggaccaatc gccccatctt tgccggtcgc 900
 gacggtgtca agaagtacgc cctgagcgag atcgagcggg aacgccgggt cggctatgcg 960
 tggtagcgcg cctgggggtga accggtcgcc cgccattatg cccagtggcg ggagcgttac 1020
 gggacgcaga aatga 1035

<210> 70
 <211> 344
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(22)

<221> DOMAIN

<222> (23)...(344)

<223> Catalytic domain

<400> 70

```

Met Ala Arg Leu Phe Arg Cys Val Cys Ala Ser Leu Gly Gly Trp Ala
 1           5           10           15
Ala Val Leu Ala Ala Ala Ala Gly Pro Asp Trp Ser Arg Leu Leu Ala
      20           25           30
Gln Pro Asp Pro Trp Phe Arg Ser Pro Ala Gly Gln Gln Ala Val Thr
      35           40           45
Asn Val Leu Ser Trp Gln Ser Ala Thr Gly Ala Trp Pro Lys Asn Leu
      50           55           60
Asp Thr Thr Arg Glu Pro Arg Arg Gln Asp Ser Ala Pro Pro Glu Gly
      65           70           75           80
Thr Phe Asp Asn Gly Ala Thr Thr Gly Glu Leu Arg Phe Leu Ala Arg
      85           90           95
Ala Phe Ala Ala Thr Gly Asp Pro Arg Cys Glu Ala Ala Val Leu Arg
      100           105           110
Gly Leu Asp Gly Ile Leu Ala Ala Gln Leu Pro Ser Gly Gly Trp Pro
      115           120           125
Gln Cys His Pro Pro Arg Ala Pro Tyr Gln Arg His Ile Thr Phe Asn
      130           135           140
Asp Gly Val Met Val Arg Ile Leu Glu Leu Leu Arg Glu Ile Asp Arg
      145           150           155           160
Ala Pro Glu Phe Arg Trp Val Asp Glu Ala Arg Arg Ala Arg Val Arg
      165           170           175
Ala Ala Phe Thr Arg Gly Leu Glu Cys Leu Leu Arg Cys Gln Val Val
      180           185           190
Val Glu Gly Arg Leu Thr Val Trp Cys Ala Gln His Asp Ala Glu Asn
      195           200           205
Phe Gln Pro Arg Pro Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly
      210           215           220
Ala Glu Ser Ala Gly Ile Leu Val Phe Leu Met Ser Leu Glu Pro Pro
      225           230           235           240
Thr Pro Glu Ile Ala Arg Ala Val Glu Ala Gly Ala Ala Trp Phe Ser
      245           250           255
Ala Val Lys Leu Glu Gly Phe Arg Leu Glu Arg Thr Ala Asp Asp Ala
      260           265           270
Arg Val Val Glu Glu Pro Gly Ala Pro Pro Leu Trp Ala Arg Phe Tyr
      275           280           285
Glu Ile Gly Thr Asn Arg Pro Ile Phe Ala Gly Arg Asp Gly Val Lys
      290           295           300
Lys Tyr Ala Leu Ser Glu Ile Glu Arg Glu Arg Arg Val Gly Tyr Ala
      305           310           315           320
Trp Tyr Gly Ala Trp Gly Glu Pro Val Ala Arg His Tyr Ala Gln Trp
      325           330           335
Arg Glu Arg Tyr Gly Thr Gln Lys
      340

```

<210> 71

<211> 1038

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 71

gtgactcgtg tcgcccttgc gatggggctt gttgcatggg ttccggcgct cgcttcagct

60

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gggcccgcgtg catatattgca gaagccggac gactgggttcg ccagtcccga ggccagggca 120
atcgccgcga acgtactcgc gcatcaggcc gatctcggcg ggtggccgaa gaacatcgac 180
acaaccgaagc cggttcaccgg cgaccggacg caaatcaaac cgaccttcga taacagcgcg 240
acaaccgacg agctccggtt tctggcgcg atccacaacg cgactcgcg cgagaagtac 300
cgcaccgcgt tgcgagaagg gctcgattac atcttgaaag cacaatacgc aaacggcggt 360
tggcgcgagt cgcacccgcc cggcaccggc taccaccggc acatcacctt caacgacaat 420
gccatggtcc gtttgatgga gctcgtgcgc gaagtgcgca cctcgaatcg gtacgacttc 480
ctggacgccc accgcccga ggcctgccgc gccgctttcg atcgcggcgt cgaatgcac 540
ctgaagtgcc agatcaaggt cgacagtaag ctgacggcat ggtgcgccc gcacgacgag 600
aaggacctcg ctccccggcc ggcgcggacc tacgagctcg tctcactcag cggctcgag 660
tcggtcggga tcgtccgcct actcatgagc ctcgatcgac caagcccga ggtcgctcgg 720
gccatcgacg gcgcggtcgc gtggttccag tcggcgaagc tcgaaggcac caaggtcgtt 780
gtcgagcgcg acccgaagta tccggcgccg cgggaacgcg tgggtgtgaa ggatccaaag 840
gcaccgccac tctggcgcg cttctacgaa atcggcacga atcgcccat cttctccgac 900
cgcgacggca tcaagaagta cgcgctcgcc gagatcgccc ccgaacggcg gaatggctat 960
gcctggtatg gcacctggcc gcgcgacctg ctggagaagg aatacccagg gtggaaaaag 1020
aagctggccc ggccgtga 1038

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<210> 72
 <211> 345
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(20)

<221> DOMAIN
 <222> (21)...(345)
 <223> Catalytic domain

<400> 72

Met	Thr	Arg	Val	Ala	Leu	Ala	Met	Gly	Leu	Val	Ala	Trp	Val	Pro	Ala
1				5					10					15	
Leu	Ala	Ser	Ala	Gly	Pro	Ala	Ala	Tyr	Leu	Gln	Lys	Pro	Asp	Asp	Trp
			20					25					30		
Phe	Ala	Ser	Pro	Glu	Ala	Arg	Ala	Ile	Ala	Ala	Asn	Val	Leu	Ala	His
		35					40					45			
Gln	Ala	Asp	Leu	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Thr	Thr	Lys	Pro
	50				55					60					
Phe	Thr	Gly	Asp	Arg	Thr	Gln	Ile	Lys	Pro	Thr	Phe	Asp	Asn	Ser	Ala
65					70					75				80	
Thr	Thr	Asp	Glu	Leu	Arg	Phe	Leu	Ala	Arg	Ile	His	Asn	Ala	Thr	Arg
				85					90					95	
Asp	Glu	Lys	Tyr	Arg	Thr	Ala	Phe	Glu	Lys	Gly	Leu	Asp	Tyr	Ile	Leu
			100					105					110		
Lys	Ala	Gln	Tyr	Ala	Asn	Gly	Gly	Trp	Pro	Gln	Ser	His	Pro	Pro	Gly
		115				120						125			
Thr	Gly	Tyr	His	Arg	His	Ile	Thr	Phe	Asn	Asp	Asn	Ala	Met	Val	Arg
	130					135					140				
Leu	Met	Glu	Leu	Val	Arg	Glu	Val	Ala	Thr	Ser	Asn	Arg	Tyr	Asp	Phe
145					150					155				160	
Leu	Asp	Ala	Asp	Arg	Arg	Lys	Ala	Cys	Arg	Ala	Ala	Phe	Asp	Arg	Gly
				165					170					175	
Ile	Glu	Cys	Ile	Leu	Lys	Cys	Gln	Ile	Lys	Val	Asp	Ser	Lys	Leu	Thr
		180					185						190		
Ala	Trp	Cys	Ala	Gln	His	Asp	Glu	Lys	Asp	Leu	Ala	Pro	Arg	Pro	Ala

	195		200		205	
Arg	Thr	Tyr	Glu	Leu	Val	Ser
	210					215
Val	Arg	Leu	Leu	Met	Ser	Leu
225					230	
Ala	Ile	Asp	Gly	Ala	Val	Ala
						245
Thr	Lys	Val	Val	Val	Glu	Arg
						260
Arg	Val	Val	Val	Lys	Asp	Pro
						275
Tyr	Glu	Ile	Gly	Thr	Asn	Arg
						290
Lys	Lys	Tyr	Ala	Leu	Ala	Glu
305						310
Ala	Trp	Tyr	Gly	Thr	Trp	Pro
						325
Gly	Trp	Lys	Lys	Lys	Leu	Ala
						340
						200
						215
						230
						245
						260
						275
						290
						305
						320
						335
						205
						220
						235
						250
						265
						280
						295
						310
						325
						340

<210> 73
 <211> 1221
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 73	
atgctcacca aaacatcact acttattgca ttgctaggca gttgttgtat cgcaccatta	60
catgcggaca caccagcaag caatgcaccg acaaccaatg catcaattcc gctacagcaa	120
actgcgagcg atgctgccgc ctggaaaaat tatctcgcca aatccaacga gttgcgcaaa	180
gcagaccagg cgcagctcaa agccgagctg aaaaaactcg ggcaaaaaac cgcgagtttg	240
cctgagtaca ccaaagaatt tggttttgaa gtgaagcagt catctgagt gtttaaaagc	300
actgaaggta aacgagtgat ggatattatc ctatcgtttc aaactccttc tggcggctgg	360
tcaaaaacgca ctgacatgag caaagcgccg cgcaaacccg gccaggcatt tgggtgtgaa	420
aaaaattaca tccccacctt tgataatggc gcgaccagca cacaattaat gctactggca	480
caggcgcatc aagccactgg cgataaacgc tacagcgatg catttgcgcg cgggcttgaa	540
tttatcatca ccgctcaata tccaatggc ggctggccac aaaattttcc attggttggc	600
aagtatcacg atcacatcac ttacaacgat gccctgatgc gcgatttaat ggtagtgcta	660
cacaagggtg ccatggccaa ggatgaattt gcctttgtat ccaaggcgca gcaacaggcc	720
gcacaagcga gcctcgaacg cgcgctggac tgcgttttga aaaccaggt gatggccaat	780
ggccaattaa ctatatgggg tgcgcagcac gatgccaaaa ccttaaaacc cgccaaagcg	840
cgcgcctatg aaatgatttc actcaccagt tctgaaagcg tgtggatgct cgatttttta	900
atggatttgc aacagcccag cgctgacatt attaaatccg tgcacgcggc tgccgcttgg	960
tatgagcaaa ataaaattat cggaaaaacc tggaccgggg gcgacacagt tctgaaagac	1020
gataaggatg caccgccaat ctgggcgcgt ttttatgaga taggtacgaa caaaccctg	1080
tttggcgacc gcgatgactc tgtccattac gatctggcaa aggtatcgga agagcgccgc	1140
acgggttatg cctggtacac aacctcacc aatcaggtat taaaaaagta cgcgcgctgg	1200
gctaaacaat atccgcaata a	1221

<210> 74
 <211> 406
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(22)

<221> DOMAIN
 <222> (23)...(406)
 <223> Catalytic domain

<400> 74
 Met Leu Thr Lys Thr Ser Leu Leu Ile Ala Leu Leu Gly Ser Cys Cys
 1 5 10 15
 Ile Ala Pro Leu His Ala Asp Thr Pro Ala Ser Asn Ala Pro Thr Thr
 20 25 30
 Asn Ala Ser Ile Pro Leu Gln Gln Thr Ala Ser Asp Ala Ala Ala Trp
 35 40 45
 Lys Asn Tyr Leu Ala Lys Ser Asn Glu Leu Arg Lys Ala Asp Gln Ala
 50 55 60
 Gln Leu Lys Ala Glu Leu Lys Lys Leu Gly Gln Lys Thr Ala Ser Leu
 65 70 75 80
 Pro Glu Tyr Thr Lys Glu Phe Gly Phe Glu Val Lys Gln Ser Ser Glu
 85 90 95
 Trp Phe Lys Ser Thr Glu Gly Lys Arg Val Met Asp Ile Ile Leu Ser
 100 105 110
 Phe Gln Thr Pro Ser Gly Gly Trp Ser Lys Arg Thr Asp Met Ser Lys
 115 120 125
 Ala Pro Arg Lys Pro Gly Gln Ala Phe Gly Val Glu Lys Asn Tyr Ile
 130 135 140
 Pro Thr Phe Asp Asn Gly Ala Thr Ser Thr Gln Leu Met Leu Leu Ala
 145 150 155 160
 Gln Ala His Gln Ala Thr Gly Asp Lys Arg Tyr Ser Asp Ala Phe Ala
 165 170 175
 Arg Gly Leu Glu Phe Ile Ile Thr Ala Gln Tyr Pro Asn Gly Gly Trp
 180 185 190
 Pro Gln Asn Phe Pro Leu Val Gly Lys Tyr His Asp His Ile Thr Tyr
 195 200 205
 Asn Asp Ala Leu Met Arg Asp Leu Met Val Val Leu His Lys Val Ala
 210 215 220
 Met Ala Lys Asp Glu Phe Ala Phe Val Ser Lys Ala Gln Gln Gln Ala
 225 230 235 240
 Ala Gln Ala Ser Leu Glu Arg Ala Leu Asp Cys Val Leu Lys Thr Gln
 245 250 255
 Val Met Ala Asn Gly Gln Leu Thr Ile Trp Gly Ala Gln His Asp Ala
 260 265 270
 Lys Thr Leu Lys Pro Ala Lys Ala Arg Ala Tyr Glu Met Ile Ser Leu
 275 280 285
 Thr Ser Ser Glu Ser Val Trp Met Leu Asp Phe Leu Met Asp Leu Gln
 290 295 300
 Gln Pro Ser Ala Asp Ile Ile Lys Ser Val His Ala Ala Ala Ala Trp
 305 310 315 320
 Tyr Glu Gln Asn Lys Ile Ile Gly Lys Thr Trp Thr Arg Gly Asp Thr
 325 330 335
 Val Leu Lys Asp Asp Lys Asp Ala Pro Pro Ile Trp Ala Arg Phe Tyr
 340 345 350
 Glu Ile Gly Thr Asn Lys Pro Leu Phe Gly Asp Arg Asp Asp Ser Val
 355 360 365
 His Tyr Asp Leu Ala Lys Val Ser Glu Glu Arg Arg Thr Gly Tyr Ala
 370 375 380
 Trp Tyr Thr Thr Ser Pro Asn Gln Val Leu Lys Lys Tyr Ala Arg Trp
 385 390 395 400
 Ala Lys Gln Tyr Pro Gln

405

<210> 75
 <211> 1767
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 75
 atgaccacaa cccgccgcac tatcctgaaa gccgccgccca gcgccggcgc gatcgccagc 60
 accggctggc ccgccttggc cgccgcacag gccgccgaag ccgccgaccc gtgggcccg 120
 gccagcaga tcatcgaccg ctctgccaag ccgctcagct tcccgaacag ggacttccc 180
 atcaccgagt tcggcgccaa accctgcaag ctggtcaaag cccagggcct ggtcgaagta 240
 agagtcaaag gcgaactcga aacgccagca ccgaagcgc cggacgccta cccggcaatc 300
 aaagccgccca tcgccgcagc gagcaaggcc ggaggagggc gcgtgctgat cccggccggc 360
 aactggtact gcaagggcc tatcgtgctg ctgtcgaaac tgcacgtgca ccttgccaag 420
 ggccgcgaag tctacttcag cgccaacgcc aaggacttcg cccgcgacgg cgactacgac 480
 tggcgcccca acggcaagct ggtgctctcg cgctggcaag gcaacgattg cctgaacttc 540
 tcgcccattg tctacgcgcg cgggcaaaag aatatcgcca ttaccggcga agactggacc 600
 agcatcctga acggccaggc cggcgtggcg ttcgaagacg gcagcggcaa tggttggtg 660
 ggcatgaacc ccgccggcgc gccgcccgcc agcaccacgc accagggcgc agccaatccg 720
 aacaacgccg aggagccaat cgccagactg cccacgcgcc acgcgaactg gagcgcgcag 780
 gacaagtacc tgccgtgct gtccgaagcc ggcggtgccg ccgagcgcgc cgtgttcgg 840
 ctggggcact acctgcggcc gtcgatggtc gaattcgctg actgcgggga tgtgctgatg 900
 cagggtacc aggtcatcaa cacgccgttc tggattcatc acccgggtcaa ctcacgcaac 960
 attcacttct ccaaagtgcg catggaaagc atcggcccga attcggacgg ttctgatccc 1020
 gagtcttgcg acaccatcct ggtggacggc tgcctgttca ataccggcga cgactgcac 1080
 gccatcaaat ccggcaagaa ccgagactcg caatacggcc caacgcgcaa tatggtggtc 1140
 cagaactgca tcatgaaccg cggccacggc ggcgttacgc tgggcagcga aatggcgggt 1200
 ggcacgcagc atatctacgc gcagaaaatc gaattccgca acgcgttctg ggaccacgac 1260
 ccgctgggca cggccatccg aatgaagacg aacatgaacc gcggcggtta ccttcgtcat 1320
 ttctacgtgc gcgacgtgac gctgccgaat ggcgtgcgta ccaagagcgg cttctacaag 1380
 acgctgccgg gatctccgct ggcaggcaag gtctccacca gcggcggcgc tgttatcact 1440
 atcgactgcg attacgcgcc gaatgacgac agcgtgcgcg tgcggccgcc gcaggtgctg 1500
 gacgtgcata tctcgaacgt ccgcgtcagc aatgtgaaaa cggccgaagg ctcttctcc 1560
 tgctaccagg ccatggtgct gctcgggccc gtggcgcca gcttcaacgg cgcgcctggc 1620
 acggccatcc tgccgatcac gaatgtcacc gtcagcgatt cggacttcgg cagcgcgcgc 1680
 aacagcgcag agccctggtt cgcgttcaac gtgcagggac tcaagctgcg caacgtgcgc 1740
 atcgatggca aggagtacaa cgtatga 1767

<210> 76
 <211> 588
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(34)

<221> DOMAIN
 <222> (110)...(555)
 <223> Catalytic domain

<400> 76
 Met Thr Thr Thr Arg Arg Thr Ile Leu Lys Ala Ala Ala Ser Ala Gly

1	5	10	15
Ala Ile Ala Ser Thr Gly Trp Pro Ala Leu Ala Ala Ala Gln Ala Ala			
	20	25	30
Gln Ala Ala Asp Pro Trp Ala Arg Ala Gln Gln Ile Ile Asp Arg Phe			
	35	40	45
Ala Lys Pro Leu Ser Phe Pro Asn Arg Asp Phe Pro Ile Thr Glu Phe			
	50	55	60
Gly Ala Lys Pro Cys Lys Leu Val Lys Ala Gln Gly Leu Val Glu Val			
65	70	75	80
Arg Val Lys Gly Glu Leu Glu Thr Pro Ala Pro Gln Ala Pro Asp Ala			
	85	90	95
Tyr Pro Ala Ile Lys Ala Ala Ile Ala Ala Ala Ser Lys Ala Gly Gly			
	100	105	110
Gly Arg Val Leu Ile Pro Ala Gly Asn Trp Tyr Cys Lys Gly Pro Ile			
	115	120	125
Val Leu Leu Ser Asn Val His Val His Leu Ala Lys Gly Ala Gln Val			
	130	135	140
Tyr Phe Ser Ala Asn Ala Lys Asp Phe Ala Arg Asp Gly Asp Tyr Asp			
145	150	155	160
Cys Gly Ala Asn Gly Lys Leu Val Leu Ser Arg Trp Gln Gly Asn Asp			
	165	170	175
Cys Leu Asn Phe Ser Pro Met Val Tyr Ala Arg Gly Gln Lys Asn Ile			
	180	185	190
Ala Ile Thr Gly Glu Asp Trp Thr Ser Ile Leu Asn Gly Gln Ala Gly			
	195	200	205
Val Ala Phe Glu Asp Gly Ser Gly Asn Gly Trp Trp Gly Met Asn Pro			
	210	215	220
Ala Gly Ala Pro Pro Gly Ser Thr Thr His Gln Gly Ala Ala Asn Pro			
225	230	235	240
Asn Asn Ala Glu Glu Pro Ile Ala Arg Leu Pro Thr Arg His Ala Asn			
	245	250	255
Trp Ser Ala Asp Asp Lys Tyr Leu Pro Leu Leu Ser Glu Ala Gly Val			
	260	265	270
Pro Ala Glu Arg Arg Val Phe Gly Leu Gly His Tyr Leu Arg Pro Ser			
	275	280	285
Met Val Glu Phe Val Asp Cys Gly Asp Val Leu Met Gln Gly Tyr Gln			
	290	295	300
Val Ile Asn Thr Pro Phe Trp Ile His His Pro Val Asn Ser Arg Asn			
305	310	315	320
Ile His Phe Ser Lys Val Arg Met Glu Ser Ile Gly Pro Asn Ser Asp			
	325	330	335
Gly Phe Asp Pro Glu Ser Cys Asp Thr Ile Leu Val Asp Gly Cys Leu			
	340	345	350
Phe Asn Thr Gly Asp Asp Cys Ile Ala Ile Lys Ser Gly Lys Asn Arg			
	355	360	365
Asp Ser Gln Tyr Gly Pro Thr Arg Asn Met Val Val Gln Asn Cys Ile			
	370	375	380
Met Asn Arg Gly His Gly Gly Val Thr Leu Gly Ser Glu Met Ala Gly			
385	390	395	400
Gly Ile Glu His Ile Tyr Ala Gln Lys Ile Glu Phe Arg Asn Ala Phe			
	405	410	415
Trp Asp His Asp Pro Leu Gly Thr Ala Ile Arg Met Lys Thr Asn Met			
	420	425	430
Asn Arg Gly Tyr Leu Arg His Phe Tyr Val Arg Asp Val Thr Leu			
	435	440	445
Pro Asn Gly Val Arg Thr Lys Ser Gly Phe Tyr Lys Thr Leu Pro Gly			
	450	455	460
Ser Pro Leu Ala Gly Lys Val Ser Thr Ser Gly Gly Ala Val Ile Thr			
465	470	475	480

Ile	Asp	Cys	Asp	Tyr 485	Ala	Pro	Asn	Asp	Asp	Ser	Val	Arg	Val	Arg	Pro
Pro	Gln	Val	Ser	Asp	Val	His	Ile	Ser	Asn	Val	Arg	Val	Ser	Asn	Val
Lys	Thr	Ala	Glu	Gly	Ser	Phe	Ser	Cys	Tyr	Gln	Ala	Met	Val	Leu	Leu
Gly	Pro	Val	Ala	Ala	Ser	Phe	Asn	Gly	Ala	Pro	Gly	Thr	Ala	Ile	Leu
Pro	Ile	Thr	Asn	Val	Thr	Val	Ser	Asp	Ser	Asp	Phe	Gly	Thr	Pro	Arg
Asn	Ser	Ala	Glu	Pro	Trp	Phe	Ala	Phe	Asn	Val	Gln	Gly	Leu	Lys	Leu
Arg	Asn	Val	Arg	Ile	Asp	Gly	Lys	Glu	Tyr	Asn	Val				

<210>	77
<211>	2043
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

[illegible]

<210> 78
 <211> 680
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(33)

<221> BINDING
 <222> (34)...(126)
 <223> Carbohydrate binding module

<221> BINDING
 <222> (199)...(322)
 <223> Carbohydrate binding module

<221> DOMAIN
 <222> (323)...(680)
 <223> Catalytic domain

<400> 78
 Met Lys Thr Ser Arg Ala Ile Phe Thr Thr Ser Thr Leu Leu His Arg
 1 5 10 15
 Ala Leu Ile Ala Ala Ser Val Ser Met Ala Met Ser Ser Ala Ala Trp
 20 25 30
 Ala Gly Cys Thr Tyr Thr Val Thr Asn Asn Trp Gly Ser Gly Phe Thr
 35 40 45
 Gly Glu Ile Lys Val Thr Asn Asn Thr Thr Ala Ser Val Asn Asn Trp
 50 55 60
 Ser Val Ser Trp Gln Glu Ser Gly Ala Ala Ile Thr Asn Ala Trp Asn
 65 70 75 80
 Ala Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Val Ser Ala Gly Trp
 85 90 95
 Asn Gly Thr Leu Ala Pro Asn Ala Ser Ala Thr Phe Gly Phe Gln Ala
 100 105 110
 Asn Gly Ser Ala Gly Ala Pro Lys Val Asn Gly Ser Leu Cys Gly Thr
 115 120 125
 Asn Thr Ser Ser Thr Pro Ala Ser Ser Ser Val Ala Ser Ser Val Lys
 130 135 140
 Ser Ser Ala Pro Val Ser Ser Ser Ser Arg Ser Ser Ser Ser Ile Ala
 145 150 155 160
 Ile Thr Ser Ser Ser Leu Ala Arg Ser Ser Ile Ala Ser Ser Ser Ser
 165 170 175
 Leu Val Ser Ser Ser Arg Ala Ser Ser Ser Ala Pro Ser Val Phe Ser
 180 185 190
 Phe Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly Ile
 195 200 205
 Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr Asn
 210 215 220
 Ala Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Ser Ala Pro
 225 230 235 240
 Ser Ser Gly Arg Tyr Thr Val Ala Phe Arg Phe Ala Asn Gly Gly Thr
 245 250 255
 Ala Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly Asn
 260 265 270

Tyr	Thr	Val	Glu	Leu	Pro	Leu	Thr	Gly	Ala	Trp	Ala	Thr	Trp	Gln	Ile
		275					280					285			
Ala	Ser	Val	Glu	Ile	Asp	Leu	Val	Gln	Gly	Asn	Asn	Ile	Leu	Lys	Leu
		290				295					300				
Ser	Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Ser	Leu	Lys	Ile
305					310					315					320
Asp	Gly	Ala	Gln	Thr	Lys	Ala	Gly	Thr	Cys	Ser	Thr	Thr	Ser	Ser	Ser
				325					330					335	
Ser	Val	Ala	Ser	Ser	Ser	Ser	Ser	Val	Lys	Ser	Ser	Ala	Ser	Ser	Ser
		340						345					350		
Ser	Ser	Ser	Ser	Thr	Ala	Ala	Lys	Ile	Leu	Thr	Leu	Asp	Gly	Asn	Pro
		355					360					365			
Ala	Ala	Ser	Trp	Phe	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Asn	Ser	Ser	Arg
		370				375					380				
Ala	Asp	Ile	Val	Leu	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys
385						390				395					400
Asn	Leu	Asp	Tyr	Asn	Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Asp	Ser
				405					410					415	
Gly	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu	Ala
			420					425						430	
Glu	Ile	Tyr	Lys	Asn	Gly	Gly	Asn	Thr	Lys	Tyr	Arg	Asp	Ala	Val	Arg
		435					440					445			
Arg	Ala	Ala	Asn	Phe	Leu	Val	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Ala	Leu
		450				455					460				
Pro	Gln	Phe	Tyr	Pro	Leu	Lys	Gly	Gly	Tyr	Ala	Asp	His	Ala	Thr	Phe
465						470				475					480
Asn	Asp	Asn	Gly	Met	Ala	Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala	Val
				485					490					495	
Asn	Lys	Arg	Ala	Pro	Phe	Asp	Asn	Asp	Ile	Phe	Ser	Asp	Ser	Asp	Arg
			500					505					510		
Ala	Lys	Phe	Lys	Thr	Ala	Val	Ala	Lys	Gly	Val	Asp	Tyr	Ile	Leu	Lys
		515					520					525			
Ala	Gln	Trp	Lys	Gln	Asn	Gly	Lys	Leu	Thr	Ala	Trp	Cys	Ala	Gln	His
		530				535					540				
Gly	Ala	Thr	Asp	Tyr	Gln	Pro	Lys	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Glu
545						550				555					560
Ser	Leu	Ser	Gly	Ser	Glu	Ser	Val	Gly	Ile	Leu	Ala	Phe	Leu	Met	Thr
				565					570					575	
Gln	Pro	Gln	Thr	Ala	Gln	Ile	Glu	Ala	Ala	Val	Lys	Ala	Gly	Val	Asn
			580					585						590	
Trp	Phe	Ala	Ser	Pro	Asn	Thr	Tyr	Leu	Ala	Asn	Tyr	Thr	Tyr	Asp	Ser
		595					600						605		
Ser	Lys	Ala	Ser	Thr	Asn	Pro	Ile	Val	Tyr	Lys	Ser	Gly	Ser	Arg	Met
		610				615					620				
Trp	Tyr	Arg	Phe	Tyr	Asp	Leu	Asn	Thr	Asn	Arg	Gly	Phe	Phe	Ser	Asp
625					630					635					640
Arg	Asp	Gly	Ser	Lys	Phe	Tyr	Asp	Ile	Thr	Gln	Met	Ser	Glu	Glu	Arg
				645					650					655	
Arg	Thr	Gly	Tyr	Ser	Trp	Gly	Gly	Ser	Tyr	Gly	Glu	Ser	Ile	Ile	Ser
			660					665						670	
Phe	Ala	Gln	Lys	Val	Gly	Tyr	Leu								
		675					680								

<210> 79

<211> 1746

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 79

atgacgacac	gacgcgaatt	catcaaaggc	tttctactta	cgggagcagc	cgtggccgctc	60
gctccgcggt	taattgcggt	cggcgcggag	gcaagtcctg	gggaaacgat	gatgccttcg	120
atcctcgcac	gcatcacacc	acctcggttt	ccgaaacgca	ccttctatct	caatcgattc	180
ggcgccaagg	gcatgaggat	cacagactgc	accgcggctt	ttcatcgcg	gatcgatgaa	240
tgcaccaaag	ccggcggttg	gaaagtcgtc	gtgcgcggcg	gcacttatct	caccggcgcg	300
attcatttga	agagcaacgt	caacctcgaa	gtctcggaag	gcgcgacgat	caagttcagt	360
caggaccgca	aacactacct	gcctgttgct	ttctcgctt	gggaagggtg	cgaagtcttc	420
aactactcgc	ctttcattta	cgcttcgaa	cagcgaaaca	tcgcgatcac	cggcaaaggc	480
acgctcgacg	gacagagtga	ttcggaacac	tgggtggcgt	ggaacggccg	tccgcagtac	540
ggatggaatg	aagggatgaa	acagcagcgt	cccgatcgca	acgcgttggt	cacaatggcg	600
gagaaaggcg	tgcgggtgcg	cgagcgcac	tttggcgaag	gtcattatct	gaggccgcag	660
ttcattcagc	cgtaccgctg	ccagaacgtg	ctgatccagg	gcgtgacgat	tccgaaactc	720
ccgatgtggg	agattcatcc	ggtgttgctg	cgcaacgtga	ctattcacga	cgtgcacatc	780
gatagtcatg	gaccaaaaca	cgacggctgc	aatcccgaat	cgtgcagcga	cgtgttgatt	840
aaggatagct	acttcgatac	cggcgacgac	tgcacgcga	tcaaatacgg	acgcaacgcc	900
gacgggcgcg	ggcttaaagc	gccgactgag	aacatcatcg	ttcaaggatg	tcgcataaaa	960
gacggccacg	gtggaatcac	ggtcggcagc	gagatctcgg	gcggcggtgc	aaacctgttt	1020
gccgagaatt	gccggctcga	cagtccaaac	ctcgatcacg	ccctgcgcgt	gaagaacaat	1080
gccatgcgcg	gcggattact	cgagaacttc	cacttccgta	acatcgaagt	cgggcagggtg	1140
gcccattgccg	tgattacgat	cgacttcaac	tacgaagagg	gcgcgaaagg	gtcgttcacg	1200
ccggtcgttc	gcgattacac	ggtcgcgcgt	ttgcgcagca	cgaagagcaa	gcacgcactc	1260
gacgtccagg	gtctgcccgg	cgcgccgggtc	atcaacctgc	gattgacaaa	ctgcacattc	1320
aacgatgtgc	agcaaccgaa	cattctcaag	aacgtcgaac	aatcaacctt	tgagaacgtc	1380
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gcaatgaccg	cgctttggcg	cgacgcgtcg	aggaaagaaa	acggttatcc	cgcgaagtgg	1500
acctatgatc	atgggctggg	cctgaaagga	atcgagcgcg	tttggaacaa	taccggcgat	1560
aagaagtatc	tgaagttcat	ccaggacagc	atggaccact	tcgtcaacga	cgacggctcc	1620
attcgcacct	acacgatcga	cgagtacaac	atcgatcacg	ttcttcccgg	acgaaacctc	1680
ctgttccttt	acaaaactac	cggtcaggaa	aagtatcgca	aagccgccgc	gttcttgcg	1740
gaacaa						1746

<210> 80

<211> 582

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(28)

<221> DOMAIN

<222> (81)...(458)

<223> Catalytic domain

<400> 80

Met	Thr	Thr	Arg	Arg	Glu	Phe	Ile	Lys	Gly	Phe	Leu	Leu	Thr	Gly	Ala
1				5					10					15	
Ala	Val	Ala	Val	Ala	Pro	Arg	Leu	Ile	Ala	Phe	Gly	Ala	Glu	Ala	Ser
		20					25						30		
Pro	Trp	Glu	Thr	Met	Met	Pro	Ser	Ile	Leu	Ala	Arg	Ile	Thr	Pro	Pro
		35					40					45			
Arg	Phe	Pro	Lys	Arg	Thr	Phe	Tyr	Leu	Asn	Arg	Phe	Gly	Ala	Lys	Gly
	50					55					60				
Asp	Gly	Val	Thr	Asp	Cys	Thr	Ala	Ala	Phe	His	Arg	Ala	Ile	Asp	Glu

65				70				75				80			
Cys	Thr	Lys	Ala	Gly	Gly	Lys	Val	Val	Val	Pro	Ala	Gly	Thr	Tyr	
				85				90				95			
Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Leu	Glu	Val	Ser
			100					105				110			
Glu	Gly	Ala	Thr	Ile	Lys	Phe	Ser	Gln	Asp	Pro	Lys	His	Tyr	Leu	Pro
		115					120					125			
Val	Val	Phe	Ser	Arg	Trp	Glu	Gly	Val	Glu	Val	Phe	Asn	Tyr	Ser	Pro
	130					135					140				
Phe	Ile	Tyr	Ala	Phe	Glu	Gln	Arg	Asn	Ile	Ala	Ile	Thr	Gly	Lys	Gly
145					150					155					160
Thr	Leu	Asp	Gly	Gln	Ser	Asp	Ser	Glu	His	Trp	Trp	Pro	Trp	Asn	Gly
			165					170						175	
Arg	Pro	Gln	Tyr	Gly	Trp	Asn	Glu	Gly	Met	Lys	Gln	Gln	Arg	Pro	Asp
		180						185					190		
Arg	Asn	Ala	Leu	Phe	Thr	Met	Ala	Glu	Lys	Gly	Val	Pro	Val	Arg	Glu
	195						200					205			
Arg	Ile	Phe	Gly	Glu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro
	210					215					220				
Tyr	Arg	Cys	Gln	Asn	Val	Leu	Ile	Gln	Gly	Val	Thr	Ile	Arg	Asn	Ser
225				230						235					240
Pro	Met	Trp	Glu	Ile	His	Pro	Val	Leu	Cys	Arg	Asn	Val	Thr	Ile	His
			245					250						255	
Asp	Val	His	Ile	Asp	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asn	Pro
		260					265						270		
Glu	Ser	Cys	Ser	Asp	Val	Leu	Ile	Lys	Asp	Ser	Tyr	Phe	Asp	Thr	Gly
	275					280						285			
Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ser	Gly	Arg	Asn	Ala	Asp	Gly	Arg	Arg
	290				295					300					
Leu	Lys	Ala	Pro	Thr	Glu	Asn	Ile	Ile	Val	Gln	Gly	Cys	Arg	Met	Lys
305				310						315					320
Asp	Gly	His	Gly	Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val
			325					330					335		
Arg	Asn	Leu	Phe	Ala	Glu	Asn	Cys	Arg	Leu	Asp	Ser	Pro	Asn	Leu	Asp
		340					345						350		
His	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Met	Arg	Gly	Gly	Leu	Leu	Glu
	355					360						365			
Asn	Phe	His	Phe	Arg	Asn	Ile	Glu	Val	Gly	Gln	Val	Ala	His	Ala	Val
	370				375						380				
Ile	Thr	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Phe	Thr
385				390					395						400
Pro	Val	Val	Arg	Asp	Tyr	Thr	Val	Asp	Arg	Leu	Arg	Ser	Thr	Lys	Ser
			405					410					415		
Lys	His	Ala	Leu	Asp	Val	Gln	Gly	Leu	Pro	Gly	Ala	Pro	Val	Ile	Asn
		420					425						430		
Leu	Arg	Leu	Thr	Asn	Cys	Thr	Phe	Asn	Asp	Val	Gln	Gln	Pro	Asn	Ile
	435					440						445			
Leu	Lys	Asn	Val	Glu	Gln	Ser	Thr	Phe	Glu	Asn	Val	Thr	Ile	Asn	Gly
	450				455					460					
Lys	Thr	Ile	Thr	Gln	Thr	Gly	Ser	Ile	Ser	Glu	Arg	Ala	Ala	Thr	Thr
465				470					475						480
Ala	Met	Thr	Ala	Leu	Trp	Arg	Asp	Ala	Ser	Arg	Lys	Glu	Asn	Gly	Tyr
			485					490					495		
Pro	Ala	Lys	Trp	Thr	Tyr	Asp	His	Gly	Leu	Val	Leu	Lys	Gly	Ile	Glu
		500					505						510		
Arg	Val	Trp	Asn	Asn	Thr	Gly	Asp	Lys	Lys	Tyr	Leu	Lys	Phe	Ile	Gln
	515					520						525			
Asp	Ser	Met	Asp	His	Phe	Val	Asn	Asp	Asp	Gly	Ser	Ile	Arg	Thr	Tyr
	530					535					540				

Thr Ile Asp Glu Tyr Asn Ile Asp His Val Leu Pro Gly Arg Asn Leu
 545 550 555 560
 Leu Phe Leu Tyr Lys Thr Thr Gly Gln Glu Lys Tyr Arg Lys Ala Ala
 565 570 575
 Ala Phe Leu Arg Glu Gln
 580

<210> 81
 <211> 1065
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 81
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 gcctgcgcgg gcgtgcggt atccgcggca gcgaccgacc cggtcgccga gaacatgctg 120
 ctgctgcaga ccgcctccgg tggctggtcc aagcactacc gcgggaagaa ggtcgactac 180
 acgcgcaatt acgacaccgc cgagcgcgcc gcgtgcgcgc cgcccgcccg gcatgacgac 240
 gcgacgatcg acaacaaggc cacgaccagc gagatcgctt acctggtgca ggcacatgcc 300
 aggacgggca acccggcgta cctcgacggt gcccgccgcg gggtcgaata cctgctgcgc 360
 gcgcagtagc cgaatggtgg ctggccgcag ttctaccccg accactcgtc ctaccggcac 420
 cagatcacgc tcaacgacga cgcgatggtg catgccatca ccgtgctgca ggacatcgcc 480
 gccggccgcg acggcatgca ggcgttgacg cccgagttcg gcgtccgcgc cgccgcccgc 540
 gcgcagcgcg gcatcggaac cctgctcgag ttgcaggtgc ggatcgacgg cgagccgacc 600
 atctgggccc cgagtagcga cgagcatagc ctgcagccgg ccaaggcccg cgcctatgaa 660
 ctgccctcgc tggccgtggc cgaatcggtc ggcgtggtgc gcctgctgat gcgccagccg 720
 aggccggatg cccggaccgt gcgcgcgac gaatcggcgg cccgctggct ggaggcgcat 780
 cgcctgcatg acctggcgct cgaacgcgct gacgcaccgg ccgaggaaac gggcaaggac 840
 gtgcgggtcg tgaccgggcc cggcgcctcg ctgtgggcgc gtttctacga cctggatgga 900
 cagcagcctc tgttcgtcga ccgcgacagc aagcccgtcc cgttcgccag cctgcccac 960
 gagcgccgca ccggctatgc ctggtacggc acctggccgg agaagctgct ggcgcaggaa 1020
 ctcccgcgct ggcgcgaggt ccatgccgcc ggcgcgcgc cctga 1065

<210> 82
 <211> 354
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(30)

<221> DOMAIN
 <222> (31)...(354)
 <223> Catalytic domain

<400> 82
 Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
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 Thr Leu Pro Val Ala Cys Ala Gly Ala Ala Val Ser Ala Ala Ala Thr
 20 25 30
 Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
 35 40 45
 Trp Ser Lys His Tyr Arg Gly Lys Lys Val Asp Tyr Thr Arg Asn Tyr
 50 55 60

Asp Thr Ala Glu Arg Ala Ala Leu Arg Ala Pro Gly Arg His Asp Asp
 65 70 75 80
 Ala Thr Ile Asp Asn Lys Ala Thr Thr Ser Glu Ile Ala Tyr Leu Val
 85 90 95
 Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
 100 105 110
 Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
 115 120 125
 Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
 130 135 140
 Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
 145 150 155 160
 Ala Gly Arg Asp Gly Met Gln Ala Leu Thr Pro Glu Phe Gly Val Arg
 165 170 175
 Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
 180 185 190
 Val Arg Ile Asp Gly Glu Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
 195 200 205
 His Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
 210 215 220
 Ala Val Ala Glu Ser Val Gly Val Val Arg Leu Leu Met Arg Gln Pro
 225 230 235 240
 Arg Pro Asp Ala Arg Thr Val Ala Ala Ile Glu Ser Ala Ala Arg Trp
 245 250 255
 Leu Glu Ala His Arg Leu His Asp Leu Ala Leu Glu Arg Val Asp Ala
 260 265 270
 Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val Val Thr Arg Pro Gly
 275 280 285
 Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Asp Gly Gln Gln Pro Leu
 290 295 300
 Phe Val Asp Arg Asp Ser Lys Pro Val Pro Phe Ala Ser Leu Pro Asn
 305 310 315 320
 Glu Arg Arg Thr Gly Tyr Ala Trp Tyr Gly Thr Trp Pro Glu Lys Leu
 325 330 335
 Leu Ala Gln Glu Leu Pro Arg Trp Arg Glu Val His Ala Ala Gly Ala
 340 345 350
 Ala Pro

<210> 83
 <211> 3618
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 83
 ttgactgctc tttcaagaaa cagtcagggt gatgtaagct gggaaccgag ttccgcccac 60
 caggtaacct acaatctaaa acgcagtacc acgaaggagg gtccttatca gaccattgct 120
 gaaaaaatgg cagaaaccga cttccgggat acagggttag agaatggcca gaagtattac 180
 tatgttgat ctgccgaaac gagtagcggg gagagtgcag attcacaagc tataacggct 240
 gtgcctgtag cgccattgca agtccgacc ggcctttcag caagtcattg caatggcggg 300
 gtaaccattc attgggaatc cgtcaatggt gccgagtctt accaagtctt gcgcagtaaa 360
 caaaagggca tcggctatga agtcatcaaa aacgggtgtaa cggaaaccag ttatacagat 420
 accgggattc ccgatggcga gaagtactat tatgtcgtat ccgccaagaa cgatacagct 480
 gaaagtgcac attcccaacc gattaacggg gctgctgtat cgacgagtgg tgtaccagcc 540
 attccaaacg gtatgaacgc tactgccggg gatggcagag ctgccttaac ctgggtccgct 600
 gtatccggcg cagattccta tagcatcaag cgcggtgagt ttaacagtgg tcaatatgag 660

gtcattgcta	aaaatataca	ctctaccggt	tatcaagata	taggccttac	aaacggtgat	720
acctatgatt	atgtgatttc	cgctgtcaat	gagcaagggg	aaagtttagg	ctccgaaccc	780
atcgccggtta	ctcctgcgaa	agtaacgggt	gtagcgaaag	aaggcggaga	ctttaaaacg	840
attcaagaag	ccattgatgc	tgcacctgat	aacagtagca	aacggcatgt	tatttttata	900
aaaaatggtc	aatatcgtga	aaagccttacg	atccctaaga	gcaaaaccaa	tctgagtttt	960
gtaggggaaa	gtaaggaagg	gaccgtgctt	gtttttaatg	ataatgcaaa	tacgcctggg	1020
ccagacggca	aaccattagg	cacttccaat	agttcaagta	tctttatcta	tgccaatgat	1080
tttattgccc	aaaatttaac	catccagaac	gactctggtc	aaggaacagg	tcaagcagtt	1140
gccgcttatg	taagggccga	tcgtctctac	tttgaaaacg	tgtagttttt	aggataccag	1200
gatacattat	atgcccatac	gggaagacag	tattataaaa	actgctacgt	agaaggggat	1260
gtggatttca	tttttgccgg	agccacagcc	ttgtttgata	cctgtcacct	tcatagcaag	1320
cgtacaggca	gtaaggttaac	cgcagctagt	accgatcaag	tcacaccgta	tgggtatggt	1380
tttttagatt	caaaaatcac	ctcagatgaa	ggcgtgacca	atgtgcatct	cgggcgacct	1440
tggcgtcctt	attcagctgt	cacctatata	aacaccgaaa	tggatgcata	gattgttcct	1500
gacggatggg	ataactgggg	gaaagtggaa	aacgagaaaa	cagccagata	ttcagaatac	1560
aataacatgg	ggccaggggc	agacccgaaa	aagcgggata	catggaccac	acaattaacg	1620
ccggagggaag	cgaatcaata	cactgtgcaa	aatgtgatga	aaggatctga	cggctgggat	1680
cctgagagaa	tcgggattat	cccattatca	ccactgtcag	caccgattat	ttcacttgat	1740
caacgagatt	ccattgtcaa	tacaccaagc	tttacaatta	caggtcaagt	ggataaagaa	1800
gcagccggtt	ctgtcaatgg	gaaggaaatt	tccttacaata	aggatggcag	cttcagcacg	1860
acggtggtgc	tgaatgacgg	tttgaacact	attacagtgg	gagctgtaga	tgtagcaggg	1920
aatcaggcta	ttcctgcagt	gttaaaaatt	gtttatgatc	atgagaaacc	tgtagtatcc	1980
atcgatgatc	ttaaaggaga	aaaaaacggg	aatcactaca	atgtaatcta	caatccgctg	2040
ccgattacag	ggaagctgaa	cgaagcagga	acagttatgg	tgaatgggtga	gaaagtaaat	2100
gtatcggaag	agttgacgtt	tagtacaata	gtcattttaa	agccgggggt	aaataacatt	2160
acgattaccg	ctgttgatca	ggcaggggaat	gaagccgaat	ctatcactat	caatgtgggt	2220
ccaaaaggga	atgctgttcc	agacgggtccc	gtcaagatta	tcaaaagtga	aacaacaaat	2280
gcaaaataccg	ttgaggttac	ttttaatagc	aagctagaaa	aatttgattc	tagtgatatt	2340
gcattgcaaa	cggctacgaa	cgtttgggca	gctctcaatc	ctggtttgaa	acaattgatg	2400
acagtggaaa	gcattaccac	aaaagtgaat	aaggataacc	aaaccgtagc	ggtgatcaaa	2460
acgaagggaag	cctttcaaga	agatggaacc	attacgctcc	caaaagttga	agatccggtt	2520
catattcaat	atttgaatgc	cgattattat	accggggatc	gtacgcagga	cattaagcat	2580
gcggatgccc	tcttaacctg	gcagatggat	catggcggtc	ggtttaaaaa	ctgggtggaa	2640
aaatataaac	ggccatggga	tgggaaagaa	ccaaaatctg	aatgggtattc	gactaatcat	2700
ggtgaactag	ggacgattga	taatgacgca	acaacaaacg	agattctctt	tttagctctg	2760
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tactcagatt	atgtgacctt	taatgataat	gcgatgggtc	gcgttatgag	tgtattaacg	2940
atggttaaaag	aaaagaagta	tccgtttaat	tccaacctag	gtgacgagca	actttctgag	3000
cagattgatg	atgcattggg	ccgtgggctg	gattatatgt	taaaatcgca	aattaaggta	3060
gacggtgaag	taaccgcatg	gtgtgctcag	catgacctg	tgacgtatga	accgaaaggg	3120
gctcgtgcgt	atgaacatcc	ttcaatctct	ggttcgggaat	ctgtagggat	tgtccagtat	3180
ttgatgtcac	tgccgaatcc	ttcaactgag	gttcaggctg	ccattcatgg	agctctaaat	3240
tggtttgaag	aggcaaaatt	ggcgggaacg	aagtatgtat	caggcgatcc	aaatgggcaa	3300
tatttctacc	cggacgccaa	cagcaatacag	tggtagcgct	tctatgaaat	tggcaccaat	3360
cgccccgattt	tctcaggaag	agacgggtgct	attaaacaca	acatcttaga	gattgaaaaa	3420
gaaagaagag	acggctaccg	ctgggcagga	gaatggccgc	aaaaattatt	aaatatcgcc	3480
aacacaactg	gctactacga	aaacagagta	tacgtagaag	tcgttgggga	tcagtctaaa	3540
aacgccgctg	gcgaatcttt	ggaaatagga	aacttatata	gaatagaggc	ctcggttcc	3600
ggttctacaa	gcaagtaa					3618

<210> 84
 <211> 1205
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (268)...(556)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (782)...(1164)
 <223> Catalytic domain

<400> 84
 Met Thr Ala Leu Ser Arg Asn Ser Gln Val Asp Val Ser Trp Glu Pro
 1 5 10 15
 Ser Ser Ala Gln Gln Val Thr Tyr Asn Leu Lys Arg Ser Thr Thr Lys
 20 25 30
 Glu Gly Pro Tyr Gln Thr Ile Ala Glu Lys Met Ala Glu Thr Asp Phe
 35 40 45
 Arg Asp Thr Gly Leu Glu Asn Gly Gln Lys Tyr Tyr Tyr Val Val Ser
 50 55 60
 Ala Glu Thr Ser Ser Gly Glu Ser Ala Asp Ser Gln Ala Ile Thr Ala
 65 70 75 80
 Val Pro Val Ala Pro Leu Gln Ala Pro Thr Gly Leu Ser Ala Ser His
 85 90 95
 Gly Asn Gly Gly Val Thr Ile His Trp Glu Ser Val Asn Gly Ala Glu
 100 105 110
 Ser Tyr Gln Val Leu Arg Ser Lys Gln Lys Gly Ile Gly Tyr Glu Val
 115 120 125
 Ile Lys Asn Gly Val Thr Glu Thr Ser Tyr Thr Asp Thr Gly Ile Pro
 130 135 140
 Asp Gly Glu Lys Tyr Tyr Tyr Val Val Ser Ala Lys Asn Asp Thr Ala
 145 150 155 160
 Glu Ser Ala Asn Ser Gln Pro Ile Asn Gly Ala Ala Val Ser Thr Ser
 165 170 175
 Gly Val Pro Ala Ile Pro Asn Gly Met Asn Ala Thr Ala Gly Asp Gly
 180 185 190
 Arg Ala Ala Leu Thr Trp Ser Ala Val Ser Gly Ala Asp Ser Tyr Ser
 195 200 205
 Ile Lys Arg Gly Glu Phe Asn Ser Gly Gln Tyr Glu Val Ile Ala Lys
 210 215 220
 Asn Ile His Ser Thr Gly Tyr Gln Asp Ile Gly Leu Thr Asn Gly Asp
 225 230 235 240
 Thr Tyr Asp Tyr Val Ile Ser Ala Val Asn Glu Gln Gly Glu Ser Leu
 245 250 255
 Gly Ser Glu Pro Ile Ala Val Thr Pro Ala Lys Val Thr Val Val Ala
 260 265 270
 Lys Glu Gly Gly Asp Phe Lys Thr Ile Gln Glu Ala Ile Asp Ala Ala
 275 280 285
 Pro Asp Asn Ser Thr Lys Arg His Val Ile Phe Ile Lys Asn Gly Gln
 290 295 300
 Tyr Arg Glu Lys Leu Thr Ile Pro Lys Ser Lys Thr Asn Leu Ser Phe
 305 310 315 320
 Val Gly Glu Ser Lys Glu Gly Thr Val Leu Val Phe Asn Asp Asn Ala
 325 330 335
 Asn Thr Pro Gly Pro Asp Gly Lys Pro Leu Gly Thr Ser Asn Ser Ser
 340 345 350
 Ser Ile Phe Ile Tyr Ala Asn Asp Phe Ile Ala Gln Asn Leu Thr Ile
 355 360 365
 Gln Asn Asp Ser Gly Gln Gly Thr Gly Gln Ala Val Ala Ala Tyr Val
 370 375 380
 Arg Ala Asp Arg Leu Tyr Phe Glu Asn Val Gln Phe Leu Gly Tyr Gln
 385 390 395 400

Asp	Thr	Leu	Tyr	Ala	His	Thr	Gly	Arg	Gln	Tyr	Tyr	Lys	Asn	Cys	Tyr	405	410	415
Val	Glu	Gly	Asp	Val	Asp	Phe	Ile	Phe	Gly	Gly	Ala	Thr	Ala	Leu	Phe	420	425	430
Asp	Thr	Cys	His	Leu	His	Ser	Lys	Arg	Thr	Gly	Ser	Lys	Leu	Thr	Ala	435	440	445
Ala	Ser	Thr	Asp	Gln	Val	Thr	Pro	Tyr	Gly	Tyr	Val	Phe	Leu	Asp	Ser	450	455	460
Lys	Ile	Thr	Ser	Asp	Glu	Gly	Val	Thr	Asn	Val	His	Leu	Gly	Arg	Pro	465	470	475
Trp	Arg	Pro	Tyr	Ser	Ala	Val	Thr	Tyr	Ile	Asn	Thr	Glu	Met	Asp	Ala	485	490	495
Ser	Ile	Val	Pro	Asp	Gly	Trp	Asp	Asn	Trp	Gly	Lys	Val	Glu	Asn	Glu	500	505	510
Lys	Thr	Ala	Arg	Tyr	Ser	Glu	Tyr	Asn	Asn	Met	Gly	Pro	Gly	Ala	Asp	515	520	525
Pro	Lys	Lys	Arg	Asp	Pro	Trp	Thr	Thr	Gln	Leu	Thr	Pro	Glu	Glu	Ala	530	535	540
Asn	Gln	Tyr	Thr	Val	Gln	Asn	Val	Met	Lys	Gly	Ser	Asp	Gly	Trp	Asp	545	550	555
Pro	Glu	Arg	Ile	Gly	Ile	Ile	Pro	Leu	Ser	Pro	Leu	Ser	Ala	Pro	Ile	565	570	575
Ile	Ser	Leu	Asp	Gln	Arg	Asp	Ser	Ile	Val	Asn	Thr	Pro	Ser	Phe	Thr	580	585	590
Ile	Thr	Gly	Gln	Val	Asp	Lys	Glu	Ala	Ala	Val	Ser	Val	Asn	Gly	Lys	595	600	605
Glu	Ile	Ser	Leu	Gln	Lys	Asp	Gly	Ser	Phe	Ser	Thr	Thr	Val	Val	Leu	610	615	620
Asn	Asp	Gly	Leu	Asn	Thr	Ile	Thr	Val	Gly	Ala	Val	Asp	Ala	Ala	Gly	625	630	635
Asn	Gln	Ala	Ile	Pro	Ala	Val	Leu	Lys	Ile	Val	Tyr	Asp	His	Glu	Lys	645	650	655
Pro	Val	Val	Ser	Ile	Asp	Asp	Leu	Lys	Gly	Glu	Lys	Asn	Gly	Asn	His	660	665	670
Tyr	Asn	Val	Ile	Tyr	Asn	Pro	Leu	Pro	Ile	Thr	Gly	Lys	Leu	Asn	Glu	675	680	685
Ala	Gly	Thr	Val	Met	Val	Asn	Gly	Glu	Lys	Val	Asn	Val	Ser	Glu	Lys	690	695	700
Leu	Thr	Phe	Ser	Thr	Lys	Val	Ile	Leu	Lys	Pro	Gly	Leu	Asn	Asn	Ile	705	710	715
Thr	Ile	Thr	Ala	Val	Asp	Gln	Ala	Gly	Asn	Glu	Ala	Glu	Ser	Ile	Thr	725	730	735
Ile	Asn	Val	Val	Pro	Lys	Gly	Asn	Ala	Val	Pro	Asp	Gly	Pro	Val	Lys	740	745	750
Ile	Ile	Lys	Ser	Glu	Thr	Thr	Asn	Ala	Asn	Thr	Val	Glu	Val	Thr	Phe	755	760	765
Asn	Ser	Lys	Leu	Glu	Lys	Phe	Asp	Ser	Ser	Asp	Ile	Ala	Leu	Gln	Thr	770	775	780
Ala	Thr	Asn	Val	Trp	Ala	Ala	Leu	Asn	Pro	Gly	Leu	Lys	Gln	Leu	Met	785	790	795
Thr	Val	Glu	Ser	Ile	Thr	Thr	Lys	Val	Asn	Lys	Asp	Asn	Gln	Thr	Val	805	810	815
Ala	Val	Ile	Lys	Thr	Lys	Glu	Ala	Phe	Gln	Glu	Asp	Gly	Thr	Ile	Thr	820	825	830
Leu	Pro	Lys	Val	Glu	Asp	Pro	Phe	His	Ile	Gln	Tyr	Leu	Asn	Ala	Asp	835	840	845
Tyr	Tyr	Thr	Gly	Asp	Arg	Thr	Gln	Asp	Ile	Lys	His	Ala	Asp	Ala	Leu	850	855	860
Leu	Thr	Trp	Gln	Met	Asp	His	Gly	Gly	Trp	Phe	Lys	Asn	Trp	Val	Glu			

865		870		875		880
Lys Tyr Lys Arg	Pro Trp Asp Gly Lys Glu	Pro Lys Ser Glu Trp Tyr				
	885	890		895		
Ser Thr Asn His	Gly Glu Leu Gly Thr Ile Asp Asn Asp Ala Thr Thr					
	900	905		910		
Asn Glu Ile Leu Phe	Leu Ala Leu Met Tyr Lys Glu Thr Gly Asp Ala					
	915	920		925		
Arg Tyr Lys Asp Ser Val	Leu Lys Gly Ile Asp Phe Leu Leu Glu Met					
	930	935		940		
Gln Val Asp Ser Gly	Gly Trp Pro Gln Val Tyr Pro Ala Arg Ser Gly					
	945	950		955		960
Tyr Ser Asp Tyr Val	Thr Phe Asn Asp Asn Ala Met Val Arg Val Met					
	965	970		975		
Ser Val Leu Thr Met	Val Lys Glu Lys Lys Tyr Pro Phe Asn Ser Asn					
	980	985		990		
Leu Gly Asp Glu Gln	Leu Ser Glu Gln Ile Asp Asp Ala Leu Gly Arg					
	995	1000		1005		
Gly Leu Asp Tyr Met	Leu Lys Ser Gln Ile Lys Val Asp Gly Glu Val					
	1010	1015		1020		
Thr Ala Trp Cys Ala	Gln His Asp Pro Val Thr Tyr Glu Pro Lys Gly					
	1025	1030		1035		1040
Ala Arg Ala Tyr Glu	His Pro Ser Ile Ser Gly Ser Glu Ser Val Gly					
	1045	1050		1055		
Ile Val Gln Tyr Leu	Met Ser Leu Pro Asn Pro Ser Thr Glu Val Gln					
	1060	1065		1070		
Ala Ala Ile His Gly	Ala Leu Asn Trp Phe Glu Glu Ala Lys Leu Ala					
	1075	1080		1085		
Gly Thr Lys Tyr Val	Ser Gly Asp Pro Asn Gly Gln Tyr Phe Tyr Pro					
	1090	1095		1100		
Asp Ala Asn Ser Asn	Thr Trp Tyr Arg Phe Tyr Glu Ile Gly Thr Asn					
	1105	1110		1115		1120
Arg Pro Ile Phe Ser	Gly Arg Asp Gly Val Ile Lys His Asn Ile Leu					
	1125	1130		1135		
Glu Ile Glu Lys Glu	Arg Arg Asp Gly Tyr Arg Trp Ala Gly Glu Trp					
	1140	1145		1150		
Pro Gln Lys Leu Leu	Asn Ile Ala Asn Thr Thr Gly Tyr Tyr Glu Asn					
	1155	1160		1165		
Arg Val Tyr Val Glu	Val Val Gly Asp Gln Ser Lys Asn Ala Ala Gly					
	1170	1175		1180		
Glu Ser Leu Glu Ile	Gly Asn Leu Tyr Arg Ile Glu Ala Ser Ala Ser					
	1185	1190		1195		1200
Gly Ser Thr Ser Lys						
	1205					

<210> 85

<211> 1152

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 85

atgtcgggttg	gaccaggtgc	taatccgaaa	gctcgtgttc	catggtccaa	acagttatcg	60
ggtgttgagg	caaagctgtt	tcagcgcgag	cggttcttca	gcctcgtctg	ggagcacact	120
tctaagaaaa	atgatcagga	agtcggcgcg	atcgcgtgga	aagatgcaca	tggaagccg	180
gatgagtgg	atgcgagtgt	tgaggcactg	cggatggccg	ataacgtcgt	tctctatcaa	240
cgcgactcag	gtggttggcc	caagaacatc	gacatggcga	aggcactcaa	cgatcgtgag	300
caggctgcga	tcctccgcca	gaagaaaaag	aacgactcca	cgatcgacaa	tggtgcgact	360

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cacacacagt tatectttct ggcgcgcgctc tatacagcac agcgtcagga gcgacatcgc 420
gagtcgtttt tcaaaggatt ggattactta ctgaatgcgc agtatccaaa tggaggctgg 480
ccgcagtttt atccgaaccc gacgggctat cacaagcaca ttacttacia cgacggtgcg 540
atgattggtg tgatgaaggt gctgcgcgat atcgtcgcgc cgaagccttt gtacgctttt 600
gtcgacgaag ctgggcgcgc gaaggcgacg agtgcagttg aaaaagggat cgagtgcatt 660
ttgaaaacgc aggtggtggt agatgggcgt cgcactgtgt ggagtgcgca acatgatgaa 720
gtaacgttag cgccagctcc tgcgcgaacc ttcgagttaa cttcgttgag cggcgggtgag 780
agcgtagata tcgttcgatt tttaatgtcg atcaaggatc cgtcgcctaa agtagttgat 840
gcggttgaat cggcgggttaa gtggtttgag caatcgaggt taaaaggcgt gaagtgggtt 900
aagaaggcgg acgcttctaa acctggcggg tttgattgag tcgtagttaa ggatccggag 960
agctcggttt gggcgcgctt ttatgagatt ggcacgaacc ggccgatctt ttccgggcgc 1020
gatggagtgg tcaaatacga cgtggcgcag atcgaacacg agcggcggac gaattatgag 1080
tggtacgttg atgaagcagc caagctgctg aagaaagagt atccggcctg gcggaaga 1140
acatctctgt ga 1152

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<210> 86
 <211> 383
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(383)
 <223> Catalytic domain

<400> 86

Met	Ser	Val	Gly	Pro	Gly	Ala	Asn	Pro	Lys	Ala	Arg	Val	Pro	Trp	Ser
1			5					10					15		
Lys	Gln	Leu	Ser	Gly	Val	Glu	Ala	Lys	Leu	Phe	Gln	Arg	Glu	Arg	Phe
		20						25					30		
Phe	Ser	Leu	Ala	Ala	Glu	His	Thr	Ser	Lys	Lys	Asn	Asp	Gln	Glu	Val
		35					40					45			
Gly	Ala	Ile	Ala	Trp	Lys	Asp	Ala	His	Gly	Lys	Pro	Asp	Glu	Trp	Tyr
	50					55					60				
Ala	Ser	Val	Glu	Ala	Leu	Arg	Met	Ala	Asp	Asn	Val	Val	Leu	Tyr	Gln
65					70					75					80
Arg	Asp	Ser	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Ala	Lys	Ala	Leu
			85					90					95		
Asn	Asp	Arg	Glu	Gln	Ala	Ala	Ile	Leu	Arg	Gln	Lys	Lys	Lys	Asn	Asp
		100						105					110		
Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	His	Thr	Gln	Leu	Ser	Phe	Leu	Ala
	115						120					125			
Arg	Val	Tyr	Thr	Ala	Gln	Arg	Gln	Glu	Arg	His	Arg	Glu	Ser	Phe	Phe
	130					135					140				
Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Asn	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp
145					150					155					160
Pro	Gln	Phe	Tyr	Pro	Asn	Pro	Thr	Gly	Tyr	His	Lys	His	Ile	Thr	Tyr
			165					170						175	
Asn	Asp	Gly	Ala	Met	Ile	Gly	Val	Met	Lys	Val	Leu	Arg	Asp	Ile	Ala
		180						185					190		
Ala	Ala	Lys	Pro	Leu	Tyr	Ala	Phe	Val	Asp	Glu	Ala	Arg	Arg	Ala	Lys
	195						200					205			
Ala	Thr	Ser	Ala	Val	Glu	Lys	Gly	Ile	Glu	Cys	Ile	Leu	Lys	Thr	Gln
	210					215					220				
Val	Val	Val	Asp	Gly	Arg	Arg	Thr	Val	Trp	Ser	Ala	Gln	His	Asp	Glu
225					230					235					240
Val	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Arg	Thr	Phe	Glu	Leu	Thr	Ser	Leu

					245					250					255
Ser	Gly	Gly	Glu	Ser	Val	Asp	Ile	Val	Arg	Phe	Leu	Met	Ser	Ile	Lys
			260					265					270		
Asp	Pro	Ser	Pro	Lys	Val	Val	Asp	Ala	Val	Glu	Ser	Ala	Val	Lys	Trp
			275				280					285			
Phe	Glu	Gln	Ser	Glu	Leu	Lys	Gly	Val	Lys	Trp	Val	Lys	Lys	Ala	Asp
			290				295				300				
Ala	Ser	Lys	Pro	Gly	Gly	Phe	Asp	Cys	Val	Val	Val	Lys	Asp	Pro	Glu
					310					315					320
Ser	Ser	Val	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile
				325					330					335	
Phe	Ser	Gly	Arg	Asp	Gly	Val	Val	Lys	Tyr	Asp	Val	Ala	Gln	Ile	Glu
				340				345					350		
His	Glu	Arg	Arg	Thr	Asn	Tyr	Glu	Trp	Tyr	Val	Asp	Glu	Ala	Ala	Lys
							360					365			
Leu	Leu	Lys	Lys	Glu	Tyr	Pro	Ala	Trp	Arg	Lys	Arg	Thr	Ser	Leu	
						375					380				

<210>	87
<211>	1698
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

[illegible]

$\langle 210 \rangle$	88
$\langle 211 \rangle$	565

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<221> DOMAIN
<222> (33)...(375)
<223> Catalytic domain

<400> 88
Met Ser Thr Thr Lys Cys Phe Asn Thr Ala Pro Gly Phe Thr Leu Lys
1 5 10 15
Ala Val Ala Ala Val Ala Met Phe Ala Gly Ser Ser Val Phe Ala
20 25 30
Ala Ala Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Ala Ala Ser Gly
35 40 45
Ser Gln Ser Phe Thr Ala Ala Asn Leu Asp Gln Leu Asn Thr Ile Val
50 55 60
Ala Asn Ala Lys Ser Gly Gly Tyr Pro Val Val Ile Thr Tyr Thr Gly
65 70 75 80
Asn Glu Asp Ser Leu Ile Asn Gln Met Ile Lys Asp His Thr Val Asp
85 90 95
Ser Ser Gly Asn Cys Pro Asn Pro Arg Trp Ser Glu Thr Tyr Arg Lys
100 105 110
Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Ile Gly Ala Asn
115 120 125
Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser Ser Asn Val
130 135 140
Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Ala Gly Ala Ser Asn Asp
145 150 155 160
Ala Asp Met Ile Arg Ile Asp Ser Gly Thr Asn Val Trp Val Asp His
165 170 175
Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser Pro Asp Gly
180 185 190
Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Asp Ser His Asn
195 200 205
Ile Thr Val Ser Tyr Asn Leu Ile Arg Asp Ser Lys Lys Val Gly Leu
210 215 220
Asp Gly Ser Ser Ser Ser Asp Ile Ala Gly Gly Arg Glu Ile Thr Phe
225 230 235 240
His His Asn Ile Tyr Lys Asn Val Asn Ala Arg Leu Pro Leu Gln Arg
245 250 255
Gly Gly Trp Thr His Met Tyr Asn Asn Leu Tyr Asp Gly Ile Thr Gly
260 265 270
Ser Gly Ile Asn Val Arg Gln Ala Gly Tyr Ala Leu Ile Glu Ser Asn
275 280 285
Trp Phe Gln Asn Ala Val Asn Pro Val Thr Cys Arg Tyr Asp Ser Ser
290 295 300
Asn Cys Gly Phe Trp Asp Leu Arg Asn Asn Asn Val Lys Ser Pro Ala
305 310 315 320
Asp Phe Ala Thr Tyr Asn Ile Thr Trp Thr Ser Gly Gly Thr Ile Asp
325 330 335
Ala Thr Asn Trp Thr Thr Thr Ala Pro Phe Pro Ile Ser Ile Pro Tyr
340 345 350
Ser Tyr Ser Pro Val Ser Pro Gln Cys Val Lys Asp Lys Leu Ala Ser

355	360	365
Val Ala Gly Val Gly Lys Asn Gly Ala Val Leu Asn Ser Ser Val Cys		
370	375	380
Gly Gly Ser Ser Ser Val Pro Ser Ser Ser Val Ala Thr Thr Ser		
385	390	395
Lys Ser Ser Ser Ser Val Ala Thr Ser Lys Ser Ser Ser Val Ala Thr		400
405	410	415
Thr Ser Ser Lys Ser Ser Ser Ser Val Val Pro Ser Ser Ser Ser		
420	425	430
Ser Ser Val Val Asn Asn Gly Ser Ile Ala Leu Thr Ala Thr Ala Thr		
435	440	445
Gly Asn Ser Ile Val Leu Ser Trp Ser Pro Asn Asn Leu Thr Leu Gly		
450	455	460
Thr Gln Glu Val Tyr Arg Asp Thr Asp Ser Asp Pro Ser Gly Arg Val		
465	470	475
Arg Ile Ala Ala Leu Ser Ser Ser Thr Arg Met Tyr Thr Asp Ala Thr		480
485	490	495
Ala Ser Ala Gly Gln Thr Phe Tyr Tyr Trp Ile Lys Asn Thr Thr Asn		
500	505	510
Gly Val Thr Thr Asn Ser Asn Ala Ala Ser Ala Ala Ile Gly Asp Ala		
515	520	525
Ala Arg Ala Ile Arg Ala Cys Ala Gly Asn Arg Gly Ser Gly Ala Arg		
530	535	540
Thr Ser Arg Ala Val Ser Thr Gly Ser Asn Pro Arg Gly Pro Ala Gly		
545	550	555
Ser His Pro Arg Ala		560
565		

<210> 89

<211> 1377

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 89

atgacgacgc	gacgcgaatt	cattcgagat	cttttggttg	gcggcgtagt	ggtcgctggt	60
gcaccgcgtt	tcctggcggt	ttcttcggtg	gcgagtcggt	gggaaacggt	gatgccttcg	120
atcctcgaac	gcatacaagg	accgcgtttt	ccgaaacgca	cgtgctatct	caaccggttt	180
ggagcaaaag	gcgacgggca	aactgattgc	acttcagctt	ttcgacgcgc	aatcgatcag	240
tggtcgaaag	cgggcggtgg	caaagtgtgc	gttccgcagg	gaatgtatct	caccggcgca	300
attcacttga	agagcaacgt	caatctcgag	atctccgaag	gcgcgacgat	caagttcagt	360
caaaacccga	aagactatct	cccgggtggt	ttttcgcggt	gggaaggcgt	cgaagtattc	420
aactactcac	ctttcatcta	cgcatttgaa	cagcagaaca	tcgcgatcac	gggcaagggc	480
acgctcgatg	ggcagagtga	taacgaacac	tggtggccat	ggaacggacg	cgccagggtac	540
ggttggaag	aagggatgag	ccaccagcgt	ccggatcgaa	acgcgctctt	tgcatggcg	600
gaaaaagggtg	tttcggttcg	cgaacgtggt	ttcggcgagg	gtcattactt	aaggccgcag	660
ttcattcagc	cgtatcgctg	ccagaacgta	ttgatcgacg	gagttacgat	acgaaactcg	720
ccgatgtggg	aaattcatcc	ggtgctgtgc	cggaatgtca	tcgtgcaaaa	cgtgcacatt	780
aacagtcatg	gaccaaacia	cgatggctgc	aatcccgaag	cgtgcactga	tgtgctgatt	840
aagaactgtt	acttcgacac	tggcgacgac	tgtatcgcgg	tcaaatcagg	acgcaacgcg	900
gacggccggc	ggcttaaagc	gccgacagag	aacgtgatcg	tgcaagactg	tcaaatgaaa	960
gatggacacg	gcgggatcac	tgctcggcagt	gagatctcag	gcgggtgtgag	aaatctgttt	1020
gcggagaact	gccggcttga	tagtccaaac	ctggaccatg	ctttgcgggt	taagaacaac	1080
gcgatgcgtg	gagggctgct	cgagaatttg	cacttccgaa	acatcgaaag	tggtcaggtg	1140
gcgcatgcag	tgatcacgat	cgattttaat	tacgaggaag	gcgcgaaagg	atcgttcacg	1200
ccggtggttc	gtgactacac	tgctgatggg	ttgcgcagca	cgcgaaagcaa	atacgcgctc	1260
gacgttcaag	gtctgtcggg	cgcgccgatc	gtaaatctgc	gtctgacgaa	ttgcacgttc	1320

gacaatgttg ccgaaggga cgtcgtgaag aatgttaagg acgcgacaat tcaaaaa

1377

<210> 90
<211> 459
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<221> DOMAIN
<222> (32)...(459)
<223> Catalytic domain

<400> 90
Met Thr Thr Arg Arg Glu Phe Ile Arg Asp Leu Leu Val Gly Gly Val
1 5 10 15
Val Val Ala Val Ala Pro Arg Phe Leu Ala Phe Ser Ser Val Ala Ser
20 25 30
Pro Trp Glu Thr Val Met Pro Ser Ile Leu Glu Arg Ile Lys Pro Pro
35 40 45
Arg Phe Pro Lys Arg Thr Cys Tyr Leu Asn Arg Phe Gly Ala Lys Gly
50 55 60
Asp Gly Gln Thr Asp Cys Thr Ser Ala Phe Arg Arg Ala Ile Asp Gln
65 70 75 80
Cys Ser Lys Ala Gly Gly Gly Lys Val Ile Val Pro Gln Gly Met Tyr
85 90 95
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu Glu Ile Ser
100 105 110
Glu Gly Ala Thr Ile Lys Phe Ser Gln Asn Pro Lys Asp Tyr Leu Pro
115 120 125
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
130 135 140
Phe Ile Tyr Ala Phe Glu Gln Gln Asn Ile Ala Ile Thr Gly Lys Gly
145 150 155 160
Thr Leu Asp Gly Gln Ser Asp Asn Glu His Trp Trp Pro Trp Asn Gly
165 170 175
Arg Ala Arg Tyr Gly Trp Lys Glu Gly Met Ser His Gln Arg Pro Asp
180 185 190
Arg Asn Ala Leu Phe Ala Met Ala Glu Lys Gly Val Ser Val Arg Glu
195 200 205
Arg Val Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro
210 215 220
Tyr Arg Cys Gln Asn Val Leu Ile Asp Gly Val Thr Ile Arg Asn Ser
225 230 235 240
Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Ile Val Gln
245 250 255
Asn Val His Ile Asn Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro
260 265 270
Glu Ser Cys Thr Asp Val Leu Ile Lys Asn Cys Tyr Phe Asp Thr Gly
275 280 285
Asp Asp Cys Ile Ala Val Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg
290 295 300
Leu Lys Ala Pro Thr Glu Asn Val Ile Val Gln Asp Cys Gln Met Lys
305 310 315 320
Asp Gly His Gly Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val

[illegible]

<210>	91
<211>	1125
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

[illegible]

<210>	92
<211>	374
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

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<221> DOMAIN
<222> (1) ... (374)
```

<400> 92


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Met Val Leu Gly Asn Asn Gly Gly Ser Leu Ser Cys Val Gln Tyr Ile
 1          5          10          15
Val Ile Val Lys Gly Pro Gly Gly Pro Arg Pro Pro Val Lys Pro Ala
 20          25          30
Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Ser Leu Val Gln Arg
 35          40          45
Pro Glu Trp Tyr Gly Ser Asp Glu Ala Ile Arg Ile Ala Asp Asn Val
 50          55          60
Leu Leu Tyr Gln Arg Asn Thr Gly Gly Trp Pro Lys Asp Ile Asp Met
 65          70          75          80
Ala Glu Pro Ile Pro Glu His Arg Lys Ser Phe Phe Leu Thr Glu Lys
 85          90          95
Glu Arg Thr Asp Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Gln
100          105          110
Leu Lys Tyr Leu Ala Arg Val Tyr Lys Ala Thr Arg Leu Glu Arg Phe
115          120          125
Lys Glu Gly Phe Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
130          135          140
Pro Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Asn Leu Arg Gly Tyr Tyr
145          150          155          160
Ala Asn Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Leu
165          170          175
Leu Gln Ser Ile Ala Lys Lys Ala Pro Glu Tyr Asp Phe Val Asp Pro
180          185          190
Ala Arg Arg Glu Lys Ala Ala Arg Ala Val Ala Lys Gly Ile Asp Cys
195          200          205
Ile Leu Lys Thr Gln Ile Arg Val Asn Gly Lys Leu Thr Ala Trp Cys
210          215          220
Ala Gln His Asp Ala Lys Thr Leu Ala Pro Ala Pro Ala Arg Ser Tyr
225          230          235          240
Glu Leu Glu Ser Ile Ser Gly Phe Glu Ser Val Gly Ile Val Arg Phe
245          250          255
Leu Met Ser Leu Glu Asn Pro Ser Pro Lys Val Ile Glu Ala Val Glu
260          265          270
Ala Ala Val Lys Trp Phe Glu Glu Val Lys Leu Thr Gly Ile Lys Val
275          280          285
Val Glu Lys Pro Asp Pro Ser Leu Pro Gly Gly Tyr Asp Arg Val Val
290          295          300
Val Glu Asp Pro Asn Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile
305          310          315          320
Gly Thr Asn Arg Pro Phe Phe Cys Gly Arg Asp Gly Ile Lys Lys Tyr
325          330          335
Ser Leu Ala Glu Ile Glu His Glu Arg Arg Val Gly Tyr Ser Trp Tyr
340          345          350
Thr Asn Ala Pro Ala Tyr Leu Ile Glu Lys Glu Tyr Pro Leu Trp Arg
355          360          365
Ala Lys His Pro Thr Lys
370

```

<210> 93

<211> 1062

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 93

gtggatccaa agaattggaa cccgaaaaaa gccgacgatt catggctcga aaagacgaaa

60

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cccgattacc ggctggtctc ctggcgcgac gttttagatc aaactcagct ctggtacgcg 120
gtcgcaggaag cgacgcgcac cgccaaccag gttttgctct ttcagcgcgga taacggcggc 180
tgggaaaaaaa acgtcgacat ggcggcgatg ctcactcaag ccgaacgaga aaaactcgtc 240
aaagaaaaaat ctcacaccga tacgaccatc gacaacggcg cgacgaccac gcagctgcgt 300
tatctggcaa aagtcatcac ggcgaaaaaac atcgaagctc ataaacagtc gttttctcaag 360
ggattggatt ttctgctcgc gatgcagtat gaaaacggag gatttccgca atattatcct 420
ttgaaaaacg attattcgcg cgagattact ttcaacgcag acgcgatgat caatgttctt 480
aaattgctgc gcgacgtggc aaaaaaagaag gaagattatt tattcgctcga cgaagaccgg 540
cgcgccagag cggaaggcgc ggtcgaaaaa ggcgctccgc tgatcttgaa aacacaggtc 600
gccatcgacg gcaaaaaaac gatctgggcg gcgcagtacg acgaaaacac tttgaaaccg 660
gcaaattgcga gaaagtgtga gccgcctcgc ctgcgttcgc gcgaatcggg cagcgtggtc 720
agatttttga tgctcgacgc caaaccgcag gaggaaaaaaa tcggagcgat cgaatcggcg 780
atcgaatggt ttcaaaaaaaa caaactgagc ggcatctcgt gggaatcgaa aagcggagaa 840
aacctggtcg tcaaagacaa agcggcgccg ccgatctggg gaagggttta tcaattcgaa 900
accatgcgcc ccatttttat cgggcgcgac gcggtgattc gctacgatgt catgcaaadc 960
gaagccgaac gccgcaacgg ctacggctgg tacacgaacg agccgaacga gcttttggac 1020
aaagattatc cgaaatggaa agagaaaatt aagaaaaatt ag 1062

```

<210> 94
 <211> 353
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(353)

```

<400> 94
Met Asp Pro Lys Asn Trp Asn Pro Lys Lys Ala Asp Asp Ser Trp Leu
1      5      10
Glu Lys Thr Lys Pro Asp Tyr Arg Leu Val Ser Trp Arg Asp Val Leu
20     25     30
Asp Gln Thr Gln Leu Trp Tyr Ala Val Asp Glu Ala Thr Arg Ile Ala
35     40     45
Asn Gln Val Leu Leu Phe Gln Arg Asp Asn Gly Gly Trp Glu Lys Asn
50     55     60
Val Asp Met Ala Ala Met Leu Thr Gln Ala Glu Arg Glu Lys Leu Val
65     70     75     80
Lys Glu Lys Ser His Thr Asp Thr Thr Ile Asp Asn Gly Ala Thr Thr
85     90     95
Thr Gln Leu Arg Tyr Leu Ala Lys Val Ile Thr Ala Lys Asn Ile Glu
100    105    110
Ala His Lys Gln Ser Phe Leu Lys Gly Leu Asp Phe Leu Leu Ala Met
115    120    125
Gln Tyr Glu Asn Gly Gly Phe Pro Gln Tyr Tyr Pro Leu Lys Asn Asp
130    135    140
Tyr Ser Arg Glu Ile Thr Phe Asn Asp Asp Ala Met Ile Asn Val Leu
145    150    155    160
Lys Leu Leu Arg Asp Val Ala Lys Lys Lys Glu Asp Tyr Leu Phe Val
165    170    175
Asp Glu Asp Arg Arg Ala Arg Ala Glu Gly Ala Val Glu Lys Gly Val
180    185    190
Arg Leu Ile Leu Lys Thr Gln Val Ala Ile Asp Gly Lys Lys Thr Ile
195    200    205
Trp Ala Ala Gln Tyr Asp Glu Asn Thr Leu Lys Pro Ala Asn Ala Arg
210    215    220
Lys Phe Glu Pro Ala Ser Leu Ala Ser Arg Glu Ser Val Ser Val Val

```

225					230				235				240				
Arg	Phe	Leu	Met	Leu	Asp	Ala	Lys	Pro	Asp	Glu	Glu	Lys	Ile	Gly	Ala		
				245					250					255			
Ile	Glu	Ser	Ala	Ile	Glu	Trp	Phe	Gln	Lys	Asn	Lys	Leu	Ser	Gly	Ile		
				260					265					270			
Arg	Trp	Glu	Ser	Lys	Ser	Gly	Glu	Asn	Leu	Val	Val	Lys	Asp	Lys	Ala		
				275					280					285			
Ala	Pro	Pro	Ile	Trp	Gly	Arg	Phe	Tyr	Gln	Phe	Glu	Thr	Met	Arg	Pro		
				290					295					300			
Ile	Phe	Ile	Gly	Arg	Asp	Ala	Val	Ile	Arg	Tyr	Asp	Val	Met	Gln	Ile		
305					310					315					320		
Glu	Ala	Glu	Arg	Arg	Asn	Gly	Tyr	Gly	Trp	Tyr	Thr	Asn	Glu	Pro	Asn		
				325					330					335			
Glu	Leu	Leu	Asp	Lys	Asp	Tyr	Pro	Lys	Trp	Lys	Glu	Lys	Ile	Lys	Lys		
				340					345					350			
Asn																	

<210>	95
<211>	1074
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400> 95						
atgacgctac	ccgttggtttc	cctgcgcgta	ctgctggcgc	tgctggccac	gtcgccggtc	60
gcctgcgcgg	gcgccgcggc	accgcgact	gcgaccgatc	cggtcgccga	gaacatgctg	120
cttctgcaga	ccgcctccgg	cggtctgtcc	aagcactacc	gcgagaagaa	ggtcgactac	180
gcgcgcgact	acgacgccgc	cgagcgcgcc	gcgctgcgcg	cgcccgaccg	gcatgacgat	240
gcgacgatcg	acaacaaggc	cacgaccacc	gagatcgccct	acctggtgca	ggcacatgcc	300
aggacgggca	atccggccta	cctcgacggc	gcgcgcgcgc	gcgtcgagta	cctgctgcgc	360
gcccagtacc	cgaacggcgg	ctggcgcgag	ttctaccctg	accattcgtc	ctaccggcac	420
cagatcacgc	tcaacgacga	tgcgatgtgt	cacgccatca	ccgtgctgca	ggacatcgcc	480
gcggggccgca	acggcatgca	ggtgctggcg	ccggagttcg	gcgtccgcgc	cgccgcggcc	540
gcgcagcgcg	gcatcgaaa	cctgctcgag	ttgcaggtgc	ggatcgccgg	ggtgccgacg	600
atatggggccg	cgcagtacga	cgagaccagc	ctgcaaccgg	ccaaggcccg	cgcgtacgaa	660
ctgccttcgc	tggccgtggc	cgaatcggtc	ggcgtggtgc	gcctgctgat	gcgccagccg	720
gcgcctgatg	cgcgcacggc	cgccgcgac	gaggcggcgg	ccgactggct	ggaggcgcac	780
cgctcgccgg	acctcgccct	ggaacgcac	gaagcccccg	ccgaggaaac	cggcaaggac	840
gtccgcgctcg	tggccagacc	gggcgcgctg	ttgtggggcg	gcttctacga	cctcgagcgg	900
caggtgccgc	tgttcgtatg	tcgcaacagc	cgtccggtgc	ccttcgcgga	gcttccaac	960
gagcgtcgta	cgggctatga	ctggtatggc	acctggccgg	aaaagctgct	ggcacaggaa	1020
ctcccgcgct	ggcgcaaggt	ccatgcggcc	agcgcggggc	ctccggccccg	ttga	1074

<210>	96
<211>	357
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

```
<221> SIGNAL
<222> (1) ... (31)

<221> DOMAIN
<222> (32) ... (357)
```

<223> Catalytic domain

<400> 96

```

Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
 1          5          10          15
Thr Ser Pro Val Ala Cys Ala Gly Ala Ala Ala Pro Ala Thr Ala Thr
 20          25          30
Asp Pro Val Ala Glu Asn Met Leu Leu Gln Thr Ala Ser Gly Gly
 35          40          45
Trp Ser Lys His Tyr Arg Glu Lys Lys Val Asp Tyr Ala Arg Asp Tyr
 50          55          60
Asp Ala Ala Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg His Asp Asp
 65          70          75          80
Ala Thr Ile Asp Asn Lys Ala Thr Thr Thr Glu Ile Ala Tyr Leu Val
 85          90          95
Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
100          105          110
Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
115          120          125
Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
130          135          140
Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
145          150          155          160
Ala Gly Arg Asn Gly Met Gln Val Leu Ala Pro Glu Phe Gly Val Arg
165          170          175
Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
180          185          190
Val Arg Ile Ala Gly Val Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
195          200          205
Thr Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
210          215          220
Ala Val Ala Glu Ser Val Gly Val Val Arg Leu Leu Met Arg Gln Pro
225          230          235          240
Ala Pro Asp Ala Arg Thr Val Ala Ala Ile Glu Ala Ala Ala Asp Trp
245          250          255
Leu Glu Ala His Arg Leu Pro Asp Leu Ala Leu Glu Arg Ile Glu Ala
260          265          270
Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val Val Ala Arg Pro Gly
275          280          285
Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Glu Arg Gln Val Pro Leu
290          295          300
Phe Val Asp Arg Asn Ser Arg Pro Val Pro Phe Ala Glu Leu Pro Asn
305          310          315          320
Glu Arg Arg Thr Gly Tyr Gly Trp Tyr Gly Thr Trp Pro Glu Lys Leu
325          330          335
Leu Ala Gln Glu Leu Pro Arg Trp Arg Lys Val His Ala Ala Ser Ala
340          345          350
Gly Ala Pro Ala Arg
355

```

<210> 97

<211> 2097

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 97

ttgaacgccg	ccggcagccg	gcggttcgcg	caactcgtcg	tcgcggatct	gcggcggtcg	60
gtgcccgcgc	tggcgccctt	ctttcgcgac	gagccgctgg	cgaggaggag	cgccgcgctc	120
cagcgcagcg	tcgatgcgat	cgtcgccgcg	gacggcaccg	gacagtttgc	gacggtgcag	180
gaggcgatca	acgccgcgcc	gcagaacacc	agcacgacca	gccgctggat	catcctcgtc	240
aaaccaggca	cgtatcgcga	ggtcgtctac	gtgcagcgctg	agaagcgctt	cgtcacgctg	300
atcggcgaag	acccggcacg	gacgacgac	acgtaccacc	tcaaagcgctc	tgacgtgggg	360
ctcgacggca	agcccatcgg	cacgtttcgc	acgccgacga	tggtggtgga	tgccgacgat	420
ttcacgatcg	agaacctcac	catcgagaac	ggggcagggc	cggtcgggtca	agcgctggcc	480
ttgcgagtgg	acggcgatcg	cgtgacgggtg	aggaacagcc	gcctgctggg	ctggcaggac	540
acgatctttc	tcaaccgtgg	gcgccactac	ttcgaggact	cgttcatcgg	cgggcagctg	600
gatttcattt	tcggcgcgcg	gacggcggtg	ttcgagcgat	gccatcttcg	cgctggcgcg	660
gacggctacc	tcacggccgc	gtccacgccc	gcggagcaac	gattcggtct	cgtgttctctg	720
aacagcatcg	tcagtggaga	agctggcgcc	cgcacgtacc	tcggtcgacc	gtggcgggcg	780
ttcgcgcacg	tggccttcat	caagacgacg	atgggcgagg	tggtgcgccc	ggtgggctgg	840
aacaactggg	accggccgga	gcgtgagaag	accgtgcgtt	ttctcgaagc	aggcaccagc	900
ggcgcggggc	gcagcgtcgc	tgccgcgcgc	gcctggggcg	gcgtcgccac	gccagccgag	960
ctcgctgac	tgacgaccga	ggtggtgctt	ggcggcaccg	acggctggga	cccgcgtcgc	1020
gtcgcctcgt	acccgtcggc	cgttcgcgcg	aacgcggcgc	cgctgccgcg	gccgcggggg	1080
cccagcgtcg	ctggcccgca	gagcccgcgc	gccttgacgt	gggaccagggt	cgcgcgccag	1140
ccagcgtcgt	ggctggccac	acccgaagcg	ctgcggattg	ccgagaacgt	gcgcctctat	1200
caacggcaca	ctggcggtcg	gccccaaaaac	ctcgacatgg	cgcagccgtt	gacggacgcc	1260
gatcgcgcg	gtctcacggc	cgatcgcgcg	ctcgacgact	cgaccatcga	caatggcgcc	1320
acgacgcggc	agatcgagtt	tctcgcccg	atcgccgcgc	ccaaccgcga	cgagcgcgcg	1380
caggcgtcga	tgctggctgg	gatcgactac	ctgctcgcg	cccagtatcc	aaacggcggc	1440
tggccgcagt	atttcccgt	ccgcaacgac	tactcgcgcc	acatcacgtt	caacgacgac	1500
gcgatgatcg	cggccgcgac	gatcctgcag	tcggtcgcg	tggcccgctc	gccgttcgcc	1560
ggcgtcgacg	cgactcgccg	ccggcgggcg	gcggaggccg	tcgcgcgcgc	ccatcgcggtg	1620
attctggcct	cgagattcgc	cgtcaacggc	cagctcactg	gctggtgcca	gcagcacgat	1680
gcacgcacgc	tggagccagc	gcgcggcgcg	acctacgagc	atccatcgat	cagtggccgc	1740
gaaaccgtga	cgatcgtcaa	tttcctgcgc	tcgatcgaac	cgcgcgaccg	ccagacccaa	1800
gccgccatcg	atgccgcgat	ggagtggctc	aaggccgtgc	agatccgcgg	ctggcgcacg	1860
gagcggcggc	ccgatccctc	aggaccgggc	ggttacgacg	tggtgatggt	ggaggacccc	1920
aacgcggcgc	cgctctgggc	ccgcttctac	gagattggca	ccaatcgctc	gatctactcg	1980
ggcggggacg	gcgtcatcaa	gtaccggctc	gccgagatcg	aaattgaacg	gcggaccggc	2040
tacagctggg	tcggaccgta	cgcgcaggcg	ctgctcgatg	aagagcgcg	gaagtaa	2097

<210> 98
 <211> 698
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (45)...(333)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (336)...(698)
 <223> Catalytic domain

<400> 98
 Met Asn Ala Ala Gly Ser Arg Arg Phe Ala Gln Leu Val Val Ala Asp
 1 5 10 15
 Leu Arg Arg Leu Val Pro Ala Leu Ala Pro Phe Phe Arg Asp Glu Pro
 20 25 30
 Leu Ala Gly Gly Val Ala Ala Leu Gln Arg Ser Val Asp Ala Ile Val
 35 40 45

Ala Ala Asp Gly Thr Gly Gln Phe Ala Thr Val Gln Glu Ala Ile Asn
 50 55 60
 Ala Ala Pro Gln Asn Thr Ser Thr Thr Ser Arg Trp Ile Ile Leu Val
 65 70 75 80
 Lys Pro Gly Thr Tyr Arg Glu Val Val Tyr Val Gln Arg Glu Lys Arg
 85 90 95
 Phe Val Thr Leu Ile Gly Glu Asp Pro Ala Arg Thr Thr Ile Thr Tyr
 100 105 110
 His Leu Lys Ala Ser Asp Val Gly Leu Asp Gly Lys Pro Ile Gly Thr
 115 120 125
 Phe Arg Thr Pro Thr Met Val Val Asp Ala Asp Asp Phe Thr Ile Glu
 130 135 140
 Asn Leu Thr Ile Glu Asn Gly Ala Gly Pro Val Gly Gln Ala Leu Ala
 145 150 155 160
 Leu Arg Val Asp Gly Asp Arg Val Thr Val Arg Asn Ser Arg Leu Leu
 165 170 175
 Gly Trp Gln Asp Thr Ile Phe Leu Asn Arg Gly Arg His Tyr Phe Glu
 180 185 190
 Asp Ser Phe Ile Gly Gly His Val Asp Phe Ile Phe Gly Gly Ala Thr
 195 200 205
 Ala Val Phe Glu Arg Cys His Leu Arg Ala Trp Arg Asp Gly Tyr Leu
 210 215 220
 Thr Ala Ala Ser Thr Pro Ala Glu Gln Arg Phe Gly Phe Val Phe Leu
 225 230 235 240
 Asn Ser Ile Val Ser Gly Glu Ala Gly Ala Arg Thr Tyr Leu Gly Arg
 245 250 255
 Pro Trp Arg Ala Phe Ala His Val Ala Phe Ile Lys Thr Thr Met Gly
 260 265 270
 Glu Val Val Arg Pro Val Gly Trp Asn Asn Trp Asp Arg Pro Glu Arg
 275 280 285
 Glu Lys Thr Val Arg Phe Leu Glu Ala Gly Thr Ser Gly Ala Gly Gly
 290 295 300
 Ser Val Ala Ala Arg Val Ala Trp Ala Arg Val Ala Thr Pro Ala Glu
 305 310 315 320
 Leu Ala Asp Leu Thr Thr Glu Val Val Leu Gly Gly Thr Asp Gly Trp
 325 330 335
 Asp Pro Arg Arg Val Ala Pro Tyr Pro Ser Ala Val Arg Ala Asn Ala
 340 345 350
 Ala Pro Leu Pro Arg Pro Pro Gly Pro Asp Val Ala Gly Pro Gln Ser
 355 360 365
 Pro Pro Ala Leu Thr Trp Asp Gln Val Ala Arg Gln Pro Ala Ser Trp
 370 375 380
 Leu Ala Thr Pro Glu Ala Leu Arg Ile Ala Glu Asn Val Arg Leu Tyr
 385 390 395 400
 Gln Arg His Thr Gly Trp Pro Lys Asn Leu Asp Met Ala Gln Pro
 405 410 415
 Leu Thr Asp Ala Asp Arg Ala Arg Leu Thr Ala Asp Arg Ala Leu Asp
 420 425 430
 Asp Ser Thr Ile Asp Asn Gly Ala Thr Thr Arg Gln Ile Glu Phe Leu
 435 440 445
 Ala Arg Ile Ala Ala Ala Asn Arg Asp Glu Arg Ala Gln Ala Ser Met
 450 455 460
 Leu Ala Gly Ile Asp Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly
 465 470 475 480
 Trp Pro Gln Tyr Phe Pro Leu Arg Asn Asp Tyr Ser Arg His Ile Thr
 485 490 495
 Phe Asn Asp Asp Ala Met Ile Ala Ala Ala Thr Ile Leu Gln Ser Val
 500 505 510
 Ala Leu Ala Arg Pro Pro Phe Ala Gly Val Asp Ala Thr Arg Arg Arg

515	520	525
Arg Ala Glu Ala Val	Ala Arg Ala His Arg	Val Ile Leu Ala Ser
530	535	540
Gln Ile Arg Val Asn Gly	Gln Leu Thr Gly Trp	Cys Gln Gln His Asp
545	550	555
Ala Arg Thr Leu Glu	Pro Ala Arg Gly Arg Thr	Tyr Glu His Pro Ser
565	570	575
Ile Ser Gly Arg Glu	Thr Val Thr Ile Val Asn	Phe Leu Arg Ser Ile
580	585	590
Glu Pro Arg Asp Arg	Gln Thr Gln Ala Ala Ile	Asp Ala Ala Met Glu
595	600	605
Trp Leu Lys Ala Val	Gln Ile Arg Gly Trp Arg	Thr Glu Arg Arg Pro
610	615	620
Asp Pro Ser Gly Pro	Gly Gly Tyr Asp Val	Val Met Val Glu Asp Pro
625	630	635
Asn Ala Ala Pro Leu	Trp Ala Arg Phe Tyr	Glu Ile Gly Thr Asn Arg
645	650	655
Pro Ile Tyr Ser Gly	Arg Asp Gly Val Ile Lys	Tyr Arg Leu Ala Glu
660	665	670
Ile Glu Ile Glu Arg	Arg Thr Gly Tyr Ser Trp	Val Gly Pro Tyr Ala
675	680	685
Gln Ala Leu Leu Asp	Glu Glu Arg Arg Lys	
690	695	

<210> 99

<211> 1782

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 99

atgttacta	ctaacagctc	tatttgcgcc	cggaaatccg	cgcgtttttc	actgactgcc	60
atggctgctg	cggtggtat	gatcgcgggc	acctctgcct	ttgcggcctc	taccggtggc	120
ttttcgacca	cggatggcgg	caatgtgtca	gggtcaaaat	cctttaccgc	ctcaagccac	180
acccaaatcc	agcaaactct	tgaggatgcc	aaagatggca	attatccggt	ggtgatcacc	240
tacaccggca	atgaggattc	actgattaac	caagtcgtcc	gggatcacac	cgtcgattct	300
tcaggcaact	gccctaaagc	gcgttggaaat	gatgcctacc	gcaaagtcga	aatcaaagaa	360
atgaccaagg	gtgtcaccat	tcagggtgcc	aatggttcgt	cggcgaattt	cggaatcgtg	420
gtgaataaat	ccagcaacgt	gattattcgc	aacatgaaga	ttggtgcact	gggcggcgct	480
aataacgatg	cggatatgat	ccgtgtggac	agcgggtgtga	acgtctggat	cgatcacaa	540
gaattattcg	ccgtgaacaa	cgagtgtaa	ggttcaccgc	atggcgatct	gacctttgaa	600
agcgcgattg	atatcaaaaa	agcctcgcaa	gatatcaccg	tgtcctacaa	cgtgattcgc	660
gacagtaaaa	aagtcggttt	ggatggctcc	agcagcagcg	atatcgccgg	cggccgcaaa	720
attactttcc	accacaatat	ctaccgcaac	gtagggtgcgc	gcttaccttt	gcagcgcggc	780
ggttgacgc	acatgtacaa	caacctgtac	gacggcatta	ccagctcggg	catcaacgtg	840
cgccaaaacg	gttatgcgtt	aattgaaagc	aactgggtcc	aaaacgcggt	taaccgggtc	900
acctgccgtt	ttgacagcag	caactgcggc	aagtgggata	tgcgcaacaa	taacatccgc	960
aaccgcgggtg	attttgcgac	ttacaacatc	acctggacca	gtggcggcac	catcgacgcc	1020
accaactgga	ccaccactgc	gcccttcctt	atcagcattc	cctacagcta	ttcaccgggt	1080
actccgcaat	gtgtgaaaga	tcgtctggcg	agttacgcgg	gtgtgggtaa	aaacggcgcg	1140
cagctgactg	cctcggcctg	cgggtgtgcg	gcacgtccca	cacctgcata	gtccacacct	1200
gcaagttcca	gctctgcggc	aaacagttcc	gctgcatacag	gcagtgtgag	tttgggtggc	1260
agtgcgggta	atgcatcggg	tgcacttaac	tggaccgtga	atgccaacat	taatgcgtg	1320
gaaatttatc	aggatacggg	ttctgatccc	cgcggacgtg	tgcgcattgc	gtcgtgcca	1380
accagcgca	ccaactacac	cgcaacaggt	ctgagcaacg	gcactaccta	ttacttctgg	1440
gtgaaatata	gcaccaccaa	taatgtgtgg	agcaactcca	atgtgttcag	cgccaagcca	1500
agttcaggta	caaccccgctc	atcatccagc	agcgcggctt	catcaacgcc	aagtgggtgca	1560

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ccggtgttaa gtggtacagg tgattaccca agcggcttct ccaagtgtgc tgatctgggt 1620
ggcacctgct cagtcgcctc gggcgatggg tgggttgccct ttggtcgcaa aggcaagtgg 1680
gtcaccacaaa aagtgtcagt cggtagctct attgcctgta ccgttgccgc gtttggatct 1740
gatccacaag gcaatcccaa taagtgttct tataaaaagt aa 1782

```

<210> 100
 <211> 593
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(35)

<221> DOMAIN
 <222> (36)...(593)
 <223> Catalytic domain

```

<400> 100
Met Phe Thr Thr Asn Ser Ser Ile Cys Ala Arg Lys Ser Ala Arg Phe
  1             5             10             15
Ser Leu Thr Ala Met Ala Ala Ala Val Ala Met Ile Ala Gly Thr Ser
      20             25             30
Ala Phe Ala Ala Ser Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Asn
      35             40             45
Val Ser Gly Ser Lys Ser Phe Thr Ala Ser Ser His Thr Gln Ile Gln
      50             55             60
Gln Ile Leu Glu Asp Ala Lys Asp Gly Asn Tyr Pro Val Val Ile Thr
      65             70             75             80
Tyr Thr Gly Asn Glu Asp Ser Leu Ile Asn Gln Val Val Arg Asp His
      85             90             95
Thr Val Asp Ser Ser Gly Asn Cys Pro Lys Ala Arg Trp Asn Asp Ala
      100            105            110
Tyr Arg Lys Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Gln
      115            120            125
Gly Ala Asn Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser
      130            135            140
Ser Asn Val Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Gly Gly Ala
      145            150            155            160
Asn Asn Asp Ala Asp Met Ile Arg Val Asp Ser Gly Val Asn Val Trp
      165            170            175
Ile Asp His Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser
      180            185            190
Pro Asp Gly Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Ala
      195            200            205
Ser Gln Asp Ile Thr Val Ser Tyr Asn Val Ile Arg Asp Ser Lys Lys
      210            215            220
Val Gly Leu Asp Gly Ser Ser Ser Ser Asp Ile Ala Gly Gly Arg Lys
      225            230            235            240
Ile Thr Phe His His Asn Ile Tyr Arg Asn Val Gly Ala Arg Leu Pro
      245            250            255
Leu Gln Arg Gly Gly Trp Thr His Met Tyr Asn Asn Leu Tyr Asp Gly
      260            265            270
Ile Thr Ser Ser Gly Ile Asn Val Arg Gln Asn Gly Tyr Ala Leu Ile
      275            280            285
Glu Ser Asn Trp Phe Gln Asn Ala Val Asn Pro Val Thr Cys Arg Phe
      290            295            300

```


Asp Ser Ser Asn Cys Gly Lys Trp Asp Leu Arg Asn Asn Asn Ile Arg
 305 310 315 320
 Asn Pro Gly Asp Phe Ala Thr Tyr Asn Ile Thr Trp Thr Ser Gly Gly
 325 330 335
 Thr Ile Asp Ala Thr Asn Trp Thr Thr Thr Ala Pro Phe Pro Ile Ser
 340 345 350
 Ile Pro Tyr Ser Tyr Ser Pro Val Thr Pro Gln Cys Val Lys Asp Arg
 355 360 365
 Leu Ala Ser Tyr Ala Gly Val Gly Lys Asn Gly Ala Gln Leu Thr Ala
 370 375 380
 Ser Ala Cys Gly Gly Ala Ala Ser Ser Thr Pro Ala Ser Ser Thr Pro
 385 390 395 400
 Ala Ser Ser Ser Ser Ala Ala Asn Ser Ser Ala Ala Ser Gly Ser Val
 405 410 415
 Ser Leu Gly Gly Ser Ala Gly Asn Ala Ser Val Ala Leu Asn Trp Thr
 420 425 430
 Val Asn Ala Asn Ile Asn Ala Leu Glu Ile Tyr Gln Asp Thr Asp Ser
 435 440 445
 Asp Pro Ala Gly Arg Val Arg Ile Ala Ser Leu Pro Thr Ser Ala Thr
 450 455 460
 Asn Tyr Thr Ala Thr Gly Leu Ser Asn Gly Thr Thr Tyr Tyr Phe Trp
 465 470 475 480
 Val Lys Tyr Arg Thr Thr Asn Asn Val Trp Ser Asn Ser Asn Val Phe
 485 490 495
 Ser Ala Lys Pro Ser Ser Gly Thr Thr Pro Ser Ser Ser Ser Ala
 500 505 510
 Ala Ser Ser Thr Pro Ser Gly Ala Pro Val Leu Ser Gly Thr Gly Asp
 515 520 525
 Tyr Pro Ser Gly Phe Ser Lys Cys Ala Asp Leu Gly Gly Thr Cys Ser
 530 535 540
 Val Ala Ser Gly Asp Gly Trp Val Ala Phe Gly Arg Lys Gly Lys Trp
 545 550 555 560
 Val Thr Lys Lys Val Ser Val Gly Ser Ser Ile Ala Cys Thr Val Ala
 565 570 575
 Ala Phe Gly Ser Asp Pro Gln Gly Asn Pro Asn Lys Cys Ser Tyr Lys
 580 585 590
 Lys

<210> 101
 <211> 1404
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 101
 atgactatag accgtcgaga attccttata gacctcatta tcggcaccgc cggcttcgca 60
 atcgaccga gtgatgcgtt cggccaagct gatccatgga aaaccgtcta tccgcaaatac 120
 ctgcgtcgca tacggccacc gaaatttccg aagcgagatt tcatcatcac tagattcggc 180
 gcaaagccgg gaaccgacag cgccgctgcg atcgcaaaag ctatcaccgc gtgcagcaag 240
 gcaggcggag gacgtgttct cgttcccgcga ggagagtttc tcaccggagc gatccatctg 300
 aaatcgaacg taaactttca cgtgtcaaaa ggcgcgacgc tgaaattctc gaccgaccgc 360
 aaggcatatc tcccgattgt acatacgcga tgggaaggaa tggagctgat gcatctgtca 420
 ccgttcattc acgcttatga gcagacgaac atcgctatca cgggtcaggg aacgctcgac 480
 ggccagggaa aatcattctt ctggaaatgg catggcaatc cggcttatgg cggcgatccg 540
 aacacgctca gccaacggcc cgctcgtgcg cggctttacg agatgatgga taagaatgtg 600
 ccggtcgcgg aacgtgtctt cggctctcga cattatctgc ggccgcagtt tattcagccg 660

```

tacaaatgca ggaacgtttt gatcgaagat gtgacgatcg tcgattcgcc gatgtgggaa 720
gttcatccgg tgctttgcga gaacgtcacg gtccgaaatg ttcacatttc atcgcatggt 780
ccgaacaatg acggatgcga tccggagtcg tgcaaggacg tactgatcga caactgtttt 840
ttcgacaccg gcgacgattg catcgcgatc aagtccggcc gcaacaatga cggtcgtcgg 900
atcaatgtcc cgaccgagaa catcatcgtc cgcaactgca caatgaaaga cggtcatggc 960
ggcatcacgg tcggcagtga gatttcggga ggcgtgcgaa atctttttgc gcacgattgt 1020
cgactcgaca gtgcggatct ctggaccgcg cttcgcgtca agaacaatgc gtcgcgaggc 1080
ggcaagctcg agaattttta ttttcggaat ataacggtcg gccagggtcg acgcgctgtg 1140
gtcgagatcg attttaatta cgaggaaggc gcgaaaggct cgtatattcc tgtcgttcga 1200
aattatgttg ttgaaggact gacatgcgcc acaggcaatc gcgccgtcga tctgcaagga 1260
ttggacaacg cgccgatcta caatgtaacg ctgcgaaact gtacgtttgg ttctgtccga 1320
aatcgtagtg ttgtgaaaaa cgttcgtgga cttcggctcg agaatgtgaa gatcggcggc 1380
aggatcgtaa acgaactggg atga 1404

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<210> 102
 <211> 467
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(28)

<221> DOMAIN
 <222> (78)...(459)
 <223> Catalytic domain

```

<400> 102
Met Thr Ile Asp Arg Arg Glu Phe Leu Ile Asp Leu Ile Ile Gly Thr
 1      5      10      15
Ala Gly Phe Ala Ile Ala Pro Ser Asp Ala Phe Gly Gln Ala Asp Pro
 20      25      30
Trp Lys Thr Val Tyr Pro Gln Ile Leu Ala Arg Ile Arg Pro Pro Lys
 35      40      45
Phe Pro Lys Arg Asp Phe Ile Ile Thr Arg Phe Gly Ala Lys Pro Gly
 50      55      60
Thr Asp Ser Ala Ala Ile Ala Lys Ala Ile Thr Ala Cys Ser Lys
 65      70      75      80
Ala Gly Gly Gly Arg Val Leu Val Pro Ala Gly Glu Phe Leu Thr Gly
 85      90      95
Ala Ile His Leu Lys Ser Asn Val Asn Phe His Val Ser Lys Gly Ala
 100     105     110
Thr Leu Lys Phe Ser Thr Asp Pro Lys Ala Tyr Leu Pro Ile Val His
 115     120     125
Thr Arg Trp Glu Gly Met Glu Leu Met His Leu Ser Pro Phe Ile Tyr
 130     135     140
Ala Tyr Glu Gln Thr Asn Ile Ala Ile Thr Gly Gln Gly Thr Leu Asp
 145     150     155     160
Gly Gln Gly Lys Ser Phe Phe Trp Lys Trp His Gly Asn Pro Ala Tyr
 165     170     175
Gly Gly Asp Pro Asn Thr Leu Ser Gln Arg Pro Ala Arg Ala Arg Leu
 180     185     190
Tyr Glu Met Met Asp Lys Asn Val Pro Val Ala Glu Arg Val Phe Gly
 195     200     205
Leu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro Tyr Lys Cys Arg
 210     215     220
Asn Val Leu Ile Glu Asp Val Thr Ile Val Asp Ser Pro Met Trp Glu

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225					230					235					240
Val	His	Pro	Val	Leu	Cys	Glu	Asn	Val	Thr	Val	Arg	Asn	Val	His	Ile
				245					250					255	
Ser	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asp	Pro	Glu	Ser	Cys	Lys
			260					265					270		
Asp	Val	Leu	Ile	Asp	Asn	Cys	Phe	Phe	Asp	Thr	Gly	Asp	Asp	Cys	Ile
		275					280					285			
Ala	Ile	Lys	Ser	Gly	Arg	Asn	Asn	Asp	Gly	Arg	Arg	Ile	Asn	Val	Pro
	290					295					300				
Thr	Glu	Asn	Ile	Ile	Val	Arg	Asn	Cys	Thr	Met	Lys	Asp	Gly	His	Gly
305					310					315					320
Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val	Arg	Asn	Leu	Phe
				325					330					335	
Ala	His	Asp	Cys	Arg	Leu	Asp	Ser	Ala	Asp	Leu	Trp	Thr	Ala	Leu	Arg
		340						345					350		
Val	Lys	Asn	Asn	Ala	Ser	Arg	Gly	Gly	Lys	Leu	Glu	Asn	Phe	Tyr	Phe
	355						360					365			
Arg	Asn	Ile	Thr	Val	Gly	Gln	Val	Ala	Arg	Ala	Val	Val	Glu	Ile	Asp
	370				375						380				
Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Tyr	Ile	Pro	Val	Val	Arg
385					390					395					400
Asn	Tyr	Val	Val	Glu	Gly	Leu	Thr	Cys	Ala	Thr	Gly	Asn	Arg	Ala	Val
			405						410					415	
Asp	Leu	Gln	Gly	Leu	Asp	Asn	Ala	Pro	Ile	Tyr	Asn	Val	Thr	Leu	Arg
		420						425				430			
Asn	Cys	Thr	Phe	Gly	Ser	Val	Arg	Asn	Arg	Ser	Val	Val	Lys	Asn	Val
	435					440					445				
Arg	Gly	Leu	Arg	Leu	Glu	Asn	Val	Lys	Ile	Gly	Gly	Arg	Ile	Val	Asn
	450				455						460				
Glu	Leu	Val													
465															

<210> 103

<211> 1101

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 103

atgaacaccg	cactgcaccg	cgatcatccg	ctgcccgtgc	tgctggcgct	gtgcctgccc	60
gcgctgcagg	cacaggccac	gcagaccgag	cccgtcgccg	agaacatgct	gctgctgcag	120
accgctccg	gcggctggtc	caagcaccac	cagggcaagg	cggtcgacta	cgccacacg	180
ttcaccgatg	ccgaacgtgc	ggcgtgcgc	gcgcccagacc	gcagggacga	tgcgacgatc	240
gacaacaagg	cgaccacgct	tgagatcgtc	gcgctgctgg	aagcccacca	gcgcaccggc	300
aatgccgcct	atctggcggc	tgccgagcgc	ggcgtggact	acctgctggc	cgcgagtagc	360
ccgaacggcg	gctggccgca	gtactacccg	gaccgttcgc	tgtaccggca	ccaggtcacc	420
ttcaacgatg	atgcgatgac	ccgcgtgctg	gagctgctgc	aggacatcgt	cgagggcaag	480
ggcgcgctgg	cgcagctgac	acccacgcac	ggcgaacgcg	ccagggccgc	gctcgacagg	540
ggcatcgctc	gcgtgctcgc	cacccaggta	cggatcgatg	gcgagctcac	gctctggggc	600
gcgcagtagc	acgaagccac	gctgcagccg	gcgaaggcgc	gctcctacga	gctgccatcg	660
ctggcggtcg	ccgaatcggt	cggggtgatg	cggtgctga	tgccgagacc	acagccgtcg	720
ccgcaggtgc	tgacggcggt	cgaggccggc	gcacgctggc	tgaggcgca	ccgatgcgc	780
gacctggccc	ggcgaaagat	cgacgcggcc	ggcgagaaa	ccggccagga	cgtggtgatc	840
gtcgccgagc	ccggcgcgtc	gctgtgggca	gccttctacg	acctgcagca	ccagcagccg	900
atgttcgtga	accgcgaagg	cgagcagggtg	gcccgtctcg	ccgacatgcc	caacgaacgc	960
cgcgctcggt	acgcctggta	tggcgtgtgg	ccggagaagc	tgctgcagca	ggagctgcca	1020
cgctggtaca	acacccatgc	cgaggcattg	cgcgcgatta	cgctgcgca	tgccgagcca	1080

aggccgccga agcggccctg a

1101

<210> 104

<211> 366

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(26)

<221> DOMAIN

<222> (27)...(366)

<223> Catalytic domain

<400> 104

```

Met Asn Thr Ala Leu His Arg Val Ile Arg Leu Pro Leu Leu Leu Ala
 1           5           10           15
Leu Cys Leu Pro Ala Leu Gln Ala Gln Ala Thr Gln Thr Glu Pro Val
           20           25           30
Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly Trp Ser Lys
           35           40           45
His His Gln Gly Lys Ala Val Asp Tyr Gly His Thr Phe Thr Asp Ala
           50           55           60
Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg Arg Asp Asp Ala Thr Ile
65           70           75           80
Asp Asn Lys Ala Thr Thr Leu Glu Ile Val Ala Leu Leu Glu Ala His
           85           90           95
Gln Arg Thr Gly Asn Ala Ala Tyr Leu Ala Ala Ala Gln Arg Gly Val
           100          105          110
Asp Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Tyr
           115          120          125
Tyr Pro Asp Arg Ser Leu Tyr Arg His Gln Val Thr Phe Asn Asp Asp
130          135          140
Ala Met Thr Arg Val Leu Glu Leu Leu Gln Asp Ile Val Glu Gly Lys
145          150          155          160
Gly Ala Leu Ala Gln Leu Thr Pro Thr His Gly Glu Arg Ala Arg Ala
           165          170          175
Ala Leu Asp Arg Gly Ile Ala Cys Val Leu Ala Thr Gln Val Arg Ile
180          185          190
Asp Gly Glu Leu Thr Leu Trp Ala Ala Gln Tyr Asp Glu Ala Thr Leu
195          200          205
Gln Pro Ala Lys Ala Arg Ser Tyr Glu Leu Pro Ser Leu Ala Val Ala
210          215          220
Glu Ser Val Gly Val Met Arg Leu Leu Met Arg Gln Pro Gln Pro Ser
225          230          235          240
Pro Gln Val Leu Thr Ala Val Glu Ala Gly Ala Arg Trp Leu Glu Ala
           245          250          255
His Arg Met Arg Asp Leu Ala Arg Arg Lys Ile Asp Ala Pro Gly Glu
260          265          270
Glu Thr Gly Gln Asp Val Val Ile Val Ala Glu Pro Gly Ala Ser Leu
275          280          285
Trp Ala Arg Phe Tyr Asp Leu Gln His Gln Gln Pro Met Phe Val Asn
290          295          300
Arg Glu Gly Glu Gln Val Ala Arg Phe Ala Asp Met Pro Asn Glu Arg
305          310          315          320
Arg Val Gly Tyr Ala Trp Tyr Gly Val Trp Pro Glu Lys Leu Leu Gln

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325 330 335
 Gln Glu Leu Pro Arg Trp Tyr Asn Thr His Ala Glu Ala Leu Arg Ala
 340 345 350
 Ile Thr Pro Ala His Ala Glu Pro Arg Pro Pro Lys Arg Pro
 355 360 365

<210> 105
 <211> 1203
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 105
 atgcaattca tcgaaacaca gcaattgggg accgccgcga aaccctgtggc gggacgagga 60
 ggcgacaggc gctttccgcg ggatcatgcc gccgtttgcg cgggccttgc cctcgccgtg 120
 tcgtcggccg agccgggtccg ggcgcagggc gcggatgcgg atgcggatgg cccactgccc 180
 aggtggaaca ggaggctggt ggatcgcccc gaggactggt tcgcctccga cgagggacag 240
 cgcgttgccg ccaacgtcct ccgctacca tccgcggaag gagcctggcc caaaaacacc 300
 aatctggccc ccaactcccct tcgccccgag gacattccct cctcgacctc cggggtggcc 360
 aacacgatcg acaatgaagc caccaccgtg cccattcggg ttttgcccg tttcgcgcaa 420
 atcaacgagg acacggccag ccgcgaggcg gtccagcgcg gattggacta tctcctcaag 480
 gcgcaatata cgaacgggtg ctggccgcag tatttcccgc tccgccgcgg ctaccactcg 540
 cacatcacct acaacgacga cgccatggtg aatgtgctcg acctgctgct ggacgtgtcg 600
 ctgggcgagg agccgttcca ttttgtggac gaggatcgcc gccagcgggc cgcgaccgcc 660
 gtggagcggg ggatcgaatg catcctccgc acccaaattc gccaggagga ccaaccacc 720
 ggctggtgcg cgcagtatga ccccgaaacc ttggccccgg cgtggggacg ggcgtacgag 780
 ccgcgctcga tttccggagc cgagaccgtc ggcgtggcgc ggtttctgat gcggctggag 840
 tcgccatcgc cgggaagccgt cgaagccatc gaggggcgca tcgcctggct cgacacggtg 900
 ggcacgcagg aattgcgtct cgaatggttc accaacagcg agggcaagcg tgaccggcgc 960
 gtggtcgagg acgcttccgt gggcaccctt tgggcgcgct tttacgaact cgaaacgaac 1020
 cgcccccttg tcgtggaccg cgacgggggtg ctccgctacg acttcgcgga actgacggcg 1080
 gagcgccgcc aaggttacag ctactacggc acttgccgg cgccattgct ggccacggaa 1140
 tatccgcgct ggcgcaggat gaacgagtc gccctgctcg agtcgtcctt catctcgcat 1200
 tga 1203

<210> 106
 <211> 400
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(43)

<221> DOMAIN
 <222> (44)...(400)
 <223> Catalytic domain

<400> 106
 Met Gln Phe Ile Glu Thr Gln Gln Leu Gly Thr Ala Ala Lys Pro Val
 1 5 10 15
 Ala Gly Arg Gly Asp Arg Arg Phe Pro Arg Val Met Pro Ala Val
 20 25 30
 Cys Ala Gly Leu Ala Leu Ala Val Ser Ser Ala Glu Pro Val Arg Ala
 35 40 45

Gln	Gly	Ala	Asp	Ala	Asp	Ala	Asp	Gly	Pro	Leu	Pro	Arg	Trp	Asn	Arg
50						55					60				
Arg	Leu	Val	Asp	Arg	Pro	Glu	Asp	Trp	Phe	Ala	Ser	Asp	Glu	Gly	Gln
65					70					75					80
Arg	Val	Ala	Ala	Asn	Val	Leu	Arg	Tyr	Gln	Ser	Ala	Glu	Gly	Ala	Trp
				85					90					95	
Pro	Lys	Asn	Thr	Asn	Leu	Ala	Ala	Thr	Pro	Leu	Arg	Pro	Glu	Asp	Ile
			100					105					110		
Pro	Ser	Ser	Thr	Ser	Gly	Val	Ala	Asn	Thr	Ile	Asp	Asn	Glu	Ala	Thr
	115					120						125			
Thr	Val	Pro	Ile	Arg	Phe	Leu	Ala	Arg	Phe	Ala	Gln	Ile	Asn	Glu	Asp
130						135					140				
Thr	Ala	Ser	Arg	Glu	Ala	Val	Gln	Arg	Gly	Leu	Asp	Tyr	Leu	Leu	Lys
145					150					155					160
Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp	Pro	Gln	Tyr	Phe	Pro	Leu	Arg	Arg
				165					170					175	
Gly	Tyr	His	Ser	His	Ile	Thr	Tyr	Asn	Asp	Asp	Ala	Met	Val	Asn	Val
			180					185					190		
Leu	Asp	Leu	Leu	Leu	Asp	Val	Ser	Leu	Gly	Glu	Glu	Pro	Phe	Asp	Phe
	195					200						205			
Val	Asp	Glu	Asp	Arg	Arg	Gln	Arg	Ala	Ala	Thr	Ala	Val	Glu	Arg	Gly
	210					215					220				
Ile	Glu	Cys	Ile	Leu	Arg	Thr	Gln	Ile	Arg	Gln	Glu	Asp	Gln	Pro	Thr
225					230					235					240
Gly	Trp	Cys	Ala	Gln	Tyr	Asp	Pro	Glu	Thr	Leu	Ala	Pro	Ala	Trp	Gly
				245					250					255	
Arg	Ala	Tyr	Glu	Pro	Pro	Ser	Ile	Ser	Gly	Ala	Glu	Thr	Val	Gly	Val
			260					265					270		
Ala	Arg	Phe	Leu	Met	Arg	Leu	Glu	Ser	Pro	Ser	Pro	Glu	Ala	Val	Glu
		275					280					285			
Ala	Ile	Glu	Gly	Ala	Ile	Ala	Trp	Leu	Asp	Thr	Val	Gly	Ile	Glu	Glu
	290					295					300				
Leu	Arg	Leu	Glu	Trp	Phe	Thr	Asn	Ser	Glu	Gly	Lys	Arg	Asp	Arg	Arg
305					310					315					320
Val	Val	Glu	Asp	Ala	Ser	Val	Gly	Thr	Leu	Trp	Ala	Arg	Phe	Tyr	Glu
				325					330					335	
Leu	Glu	Thr	Asn	Arg	Pro	Leu	Phe	Val	Asp	Arg	Asp	Gly	Val	Leu	Arg
			340					345					350		
Tyr	Asp	Phe	Ala	Glu	Leu	Thr	Ala	Glu	Arg	Arg	Gln	Gly	Tyr	Ser	Tyr
	355					360						365			
Tyr	Gly	Thr	Trp	Pro	Ala	Pro	Leu	Leu	Ala	Thr	Glu	Tyr	Pro	Arg	Trp
	370					375					380				
Arg	Arg	Met	Asn	Glu	Ser	Ala	Leu	Leu	Glu	Ser	Ser	Phe	Ile	Ser	His
385					390					395					400

<210> 107

<211> 1074

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 107

atgacgctac	ccgttgtttc	cctgcgcgta	ctgctggcgc	tgctggccac	gtcgccggtc	60
gcctgcgcgg	gcgctgcggc	acccgcgact	gcgaccgatc	cggtcgccga	gaacatgctg	120
cttctgcaga	ccgcctccgg	cggttggtcc	aagcactacc	gcgagaagaa	ggtcgactac	180
gcgcgcgact	acgacgccgc	cgagcgcgcc	gcgctgcgcg	cgccccgaccg	gcatgacgat	240
gccacgatcg	acaacaaggc	cacgaccacc	gagatcgcat	acctggtgca	ggcacatgcc	300

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aggacgggca atccggccta cctcgacggc ggcgcgcgcg gcgtcgagta cctgctgcgc 360
gcgcagtacc cgaacggcgg ctggccgcag ttctaccccg accattcgtc ctaccggcac 420
cagatcacgc tcaacgacga tgcgatggtg cacgccatca ccgtgctgca ggacatcgcc 480
gcggggccgca acggcatgca ggtgctggcg ccggagttcg gcgtccgcgc cgccgcggcc 540
gcgcagcgcg gcatcggaaa cctgctcgag ttgcaggtgc ggatcgacgg ggtgccgacg 600
atctgggccc cgcagtacga cgagaccacc ctgcaaccgg ccaaggcccg tgcgtacgag 660
ttgccctcgc tggccgtggc cgaatcgggtg ggcgtgatgc gcctgctgat gcgccagccg 720
gggcctgatg cgcgcacgat cgccgcgacg gaggcggcgg cggactggct ggaggcgcac 780
cgccctgccg acctcgccct ggaacgcac gaagccccg ccgaggaaac cggcaaggac 840
gtccgcgtcg tggccagacc gggcgcgtcg ttgtgggcgc gcttctacga cctcgagcgg 900
caggtgccgc tgttcgtcga tcgcaacagc cgcccggttc cattcgccga gcttcccaac 960
gagcgtcgta ccggctatgg ctggtatggc acctggccgg aaaagctgct ggcacaggaa 1020
ctcccgcgct ggcgcaaggt ccatgcggcc agcgcgggcg ctccggcccg ttga 1074

```

<210> 108
 <211> 357
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(31)

<221> DOMAIN
 <222> (32)...(357)
 <223> Catalytic domain

```

<400> 108
Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
1          5          10          15
Thr Ser Pro Val Ala Cys Ala Gly Ala Ala Ala Pro Ala Thr Ala Thr
20          25          30
Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
35          40          45
Trp Ser Lys His Tyr Arg Glu Lys Lys Val Asp Tyr Ala Arg Asp Tyr
50          55          60
Asp Ala Ala Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg His Asp Asp
65          70          75          80
Ala Thr Ile Asp Asn Lys Ala Thr Thr Thr Glu Ile Ala Tyr Leu Val
85          90          95
Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
100         105         110
Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
115         120         125
Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
130         135         140
Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
145         150         155         160
Ala Gly Arg Asn Gly Met Gln Val Leu Ala Pro Glu Phe Gly Val Arg
165         170         175
Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
180         185         190
Val Arg Ile Asp Gly Val Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
195         200         205
Thr Thr Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
210         215         220
Ala Val Ala Glu Ser Val Gly Val Met Arg Leu Leu Met Arg Gln Pro

```

225		230		235		240									
Gly	Pro	Asp	Ala	Arg	Thr	Ile	Ala	Ala	Ile	Glu	Ala	Ala	Ala	Asp	Trp
				245					250					255	
Leu	Glu	Ala	His	Arg	Leu	Pro	Asp	Leu	Ala	Leu	Glu	Arg	Ile	Glu	Ala
			260					265					270		
Pro	Ala	Glu	Glu	Thr	Gly	Lys	Asp	Val	Arg	Val	Val	Ala	Arg	Pro	Gly
		275					280					285			
Ala	Ser	Leu	Trp	Ala	Arg	Phe	Tyr	Asp	Leu	Glu	Arg	Gln	Val	Pro	Leu
	290					295					300				
Phe	Val	Asp	Arg	Asn	Ser	Arg	Pro	Val	Pro	Phe	Ala	Glu	Leu	Pro	Asn
305				310						315					320
Glu	Arg	Arg	Thr	Gly	Tyr	Gly	Trp	Tyr	Gly	Thr	Trp	Pro	Glu	Lys	Leu
			325					330						335	
Leu	Ala	Gln	Glu	Leu	Pro	Arg	Trp	Arg	Lys	Val	His	Ala	Ala	Ser	Ala
		340						345					350		
Gly	Ala	Pro	Ala	Arg											
		355													

<210> 109

<211> 1422

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 109

atgacgacac	gacgcgaatt	catcaaaggc	tttctactta	ccggagcagc	cgtggccgctc	60
gctccgcggtt	tgcttgcggtt	cgccgcggag	gcaagtccgt	gggaaacgat	gatgccttcg	120
atcctcgcac	gcatcagacc	acctcgtttt	ccgaaacgca	ccttctatct	caatcgattc	180
ggcgccaagg	gtgatggagt	cacagactgc	accgcggctt	ttcatcgccg	gatcgatgaa	240
tgcaccaaag	ccggcgggtg	gaaagtcgtc	gtgccggcgg	gcacttatct	caccggcgcg	300
attcatttga	agagcaacgt	caacctcgaa	gtctcggaag	gcgcgacgat	caagttcagt	360
caggaccgga	aactactcct	gcctgttgct	ttctcgcggt	gggaagggtg	cgaagtcttc	420
aactactcgc	ctttcattta	cgcgttcgaa	cagcgaaaca	tcgcgatcac	cggcaaaggc	480
acgctcgacg	gacagagtga	ttcggaacac	tggtggccgt	ggaacggccg	tccgcagtac	540
ggatggaaaag	aagggatgaa	acagcagcgt	cccgatcgca	acgcgttggt	cacaatggcg	600
gagaaaggcg	tgccgggtgcg	cgagcgcata	tttggcgaag	gtcattatct	gaggccgcag	660
ttcatttcagc	cgtaccgctg	ccagaacgtg	ctgatccagg	gcgtgacgat	tccgaactcg	720
ccgatgtggg	agattcatcc	ggtgttggtg	cgtaacgtga	ctattcacga	cgtgcacatc	780
gatagtcagt	gaccaaaca	cgacggctgc	aatcccgaat	cgtgcagcga	cgtgttgatt	840
aaggatagct	acttcgatac	cggcgacgac	tgcatcgcca	tcaaatacgg	acgcaacgcc	900
gacgggcggc	ggcttaaagc	gccgactgag	aacatcatcg	ttcaaggatg	tcgcatgaaa	960
gacggccacg	gtggaatcac	ggtcggcgag	gagatctcgg	gcggcgtgcg	aaacctgttt	1020
gccgagaatt	gccggctcga	cagtccaaac	ctcgatcacg	ccctgcgcgt	gaagaacaat	1080
gccatgcgcg	gcggattact	cgagaacttc	cacttccgta	acatcgaaat	cgggcagggtg	1140
gcccattgccg	tgattacgat	cgacttcaac	tacgaagagg	gcgcgaaagg	gtcgttcacg	1200
ccggtcgttc	gcgattacac	ggtcgatcgt	ttgcgcagca	cgaagagcaa	gcacgcactc	1260
gacgtccagg	gtctgcccgg	cgcgcgggtc	atcaactcgc	gattgacgaa	ctgcacattc	1320
aacgatgtgc	agcaaccgaa	cattctcaag	aacgtcgaac	aatcaacctt	tgaaaacgtc	1380
acgattaacg	gaaagacgat	cacacaaaca	ggatccaaag	aa		1422

<210> 110

<211> 474

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(21)

<221> DOMAIN

<222> (28)...(308)

<223> Pectin methyl esterase domain

<221> DOMAIN

<222> (309)...(637)

<223> Catalytic domain

<400> 110

Met	Thr	Thr	Arg	Arg	Glu	Phe	Ile	Lys	Gly	Phe	Leu	Leu	Thr	Gly	Ala	1	5	10	15
Ala	Val	Ala	Val	Ala	Pro	Arg	Leu	Leu	Ala	Phe	Ala	Ala	Glu	Ala	Ser	20	25	30	
Pro	Trp	Glu	Thr	Met	Met	Pro	Ser	Ile	Leu	Ala	Arg	Ile	Arg	Pro	Pro	35	40	45	
Arg	Phe	Pro	Lys	Arg	Thr	Phe	Tyr	Leu	Asn	Arg	Phe	Gly	Ala	Lys	Gly	50	55	60	
Asp	Gly	Val	Thr	Asp	Cys	Thr	Ala	Ala	Phe	His	Arg	Ala	Ile	Asp	Glu	65	70	75	80
Cys	Thr	Lys	Ala	Gly	Gly	Lys	Val	Val	Val	Pro	Ala	Gly	Thr	Tyr		85	90	95	
Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Leu	Glu	Val	Ser	100	105	110	
Glu	Gly	Ala	Thr	Ile	Lys	Phe	Ser	Gln	Asp	Pro	Lys	His	Tyr	Leu	Pro	115	120	125	
Val	Val	Phe	Ser	Arg	Trp	Glu	Gly	Val	Glu	Val	Phe	Asn	Tyr	Ser	Pro	130	135	140	
Phe	Ile	Tyr	Ala	Phe	Glu	Gln	Arg	Asn	Ile	Ala	Ile	Thr	Gly	Lys	Gly	145	150	155	160
Thr	Leu	Asp	Gly	Gln	Ser	Asp	Ser	Glu	His	Trp	Trp	Pro	Trp	Asn	Gly	165	170	175	
Arg	Pro	Gln	Tyr	Gly	Trp	Lys	Glu	Gly	Met	Lys	Gln	Gln	Arg	Pro	Asp	180	185	190	
Arg	Asn	Ala	Leu	Phe	Thr	Met	Ala	Glu	Lys	Gly	Val	Pro	Val	Arg	Glu	195	200	205	
Arg	Ile	Phe	Gly	Glu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro	210	215	220	
Tyr	Arg	Cys	Gln	Asn	Val	Leu	Ile	Gln	Gly	Val	Thr	Ile	Arg	Asn	Ser	225	230	235	240
Pro	Met	Trp	Glu	Ile	His	Pro	Val	Leu	Cys	Arg	Asn	Val	Thr	Ile	His	245	250	255	
Asp	Val	His	Ile	Asp	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asn	Pro	260	265	270	
Glu	Ser	Cys	Ser	Asp	Val	Leu	Ile	Lys	Asp	Ser	Tyr	Phe	Asp	Thr	Gly	275	280	285	
Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ser	Gly	Arg	Asn	Ala	Asp	Gly	Arg	Arg	290	295	300	
Leu	Lys	Ala	Pro	Thr	Glu	Asn	Ile	Ile	Val	Gln	Gly	Cys	Arg	Met	Lys	305	310	315	320
Asp	Gly	His	Gly	Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val	325	330	335	
Arg	Asn	Leu	Phe	Ala	Glu	Asn	Cys	Arg	Leu	Asp	Ser	Pro	Asn	Leu	Asp	340	345	350	
His	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Met	Arg	Gly	Gly	Leu	Leu	Glu	355	360	365	

Asn Phe His Phe Arg Asn Ile Glu Val Gly Gln Val Ala His Ala Val
 370 375 380
 Ile Thr Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Phe Thr
 385 390 395 400
 Pro Val Val Arg Asp Tyr Thr Val Asp Arg Leu Arg Ser Thr Lys Ser
 405 410 415
 Lys His Ala Leu Asp Val Gln Gly Leu Pro Gly Ala Pro Val Ile Asn
 420 425 430
 Leu Arg Leu Thr Asn Cys Thr Phe Asn Asp Val Gln Gln Pro Asn Ile
 435 440 445
 Leu Lys Asn Val Glu Gln Ser Thr Phe Glu Asn Val Thr Ile Asn Gly
 450 455 460
 Lys Thr Ile Thr Gln Thr Gly Ser Lys Glu
 465 470

<210> 111
 <211> 1440
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 111
 atgcaaaatc gtcgagaatt tttaacaactt ttatttgccg gtgccggtgc cggacttggtt 60
 ttgccgcaga tttcttttcg gcagactaaa caagccgacg cctggacgac cgagtatccg 120
 aagatttttag ccagaatcaa accgccgaaa tttcgcaaaa aagattttcc gatcaccaaa 180
 tatggagccg ttgcggacgg gaaaaccctg gcgaccgaaa gcatcaaaaa agccatcgaa 240
 gcgtgcgcca aatcggggcg cgggcgcgtc gtctgtcccc agggagaatt tttgaccggc 300
 gcgattcatt tgaaatcaaa cgtcaatctg cacatcacga aaggcgcgac cgtcaaattt 360
 tccaccaacc cgaaagatta tctgccgatc gttcacacgc gctgggaagg gatggaattg 420
 atgcatattt cgcctttaat ttatgcctac gagcaaacca acatcgccgt caccggcgag 480
 ggaacgctcg acgggcaggg caaggctttt ttctggaaat ggcacggaaa cccgcgctac 540
 ggcggaaatc cggatgtgat cagccagcgt ccggcgcgcg cccggctgta tgaaatgatg 600
 gaaaaaggcg tgcctgtggc ggagcggatt ttcggcgaaa ctacgtatct tcgcccgcag 660
 tttatccagc cctataaatg caaaaatgtt ttgatcgaa gctgttaaaat catcgattcg 720
 ccgatgtggg aagttcaccc cgttttgtgc gaaaacgtga cgatccgaaa acttcatatt 780
 tctaccacg gaccgaacaa cgacgggtgc gatccggaaa gctgcaagga cgttttgatc 840
 gaagactgct atttcgacac cggcgacgat tgcattgcca tcaaggcggg gcgcaatgaa 900
 gacgggcgac gcatcaatgt tccgaccgaa aacgtcgtcg tgcgcgggtg cgtgatgaag 960
 gacggtcacg gcggaatcac catcggaagc gagatttccg gcggcgtgcg aaatgttttc 1020
 gcggaataca accggctcga cagcgcggat ttgtggactg cgctgagagt gaaaaacaac 1080
 gcttcgcgcg gcggaataact ggagaatttt tacttccgcg atatcaccgt cgggcaggtc 1140
 tcgcgcgcgg tcgtcgaaat agattttaat tacgaggaag gcgctaaagg aaaacacacg 1200
 ccggtcgttc gcaattacgt ggtcgaaaat ctaacctgca ataaaggcaa tcgagcggtc 1260
 gatctgcagg gcttgacaa cgccccgatt tacgacatca cgatgaaaaa ctgtacgttt 1320
 aacgtggtcg aaaagccgag cgctcgtgaaa aacgtcaaa gcgtaaaact ggaaaacgtg 1380
 aagattaacg gcaaagtcgt cgagagtctg gaaaatgctg caacgacggc taaaaaataa 1440

<210> 112
 <211> 479
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(27)

<221> DOMAIN

<222> (82)...(461)

<223> Catalytic domain

<400> 112

```

Met  Gln  Asn  Arg  Arg  Glu  Phe  Leu  Gln  Leu  Leu  Phe  Ala  Gly  Ala  Gly
 1      5      10      15
Ala  Gly  Leu  Val  Leu  Pro  Gln  Ile  Ser  Phe  Gly  Gln  Thr  Lys  Gln  Ala
      20      25      30
Asp  Ala  Trp  Thr  Thr  Glu  Tyr  Pro  Lys  Ile  Leu  Ala  Arg  Ile  Lys  Pro
      35      40      45
Pro  Lys  Phe  Arg  Lys  Lys  Asp  Phe  Pro  Ile  Thr  Lys  Tyr  Gly  Ala  Val
      50      55      60
Ala  Asp  Gly  Lys  Thr  Leu  Ala  Thr  Glu  Ser  Ile  Lys  Lys  Ala  Ile  Glu
65      70      75      80
Ala  Cys  Ala  Lys  Ser  Gly  Gly  Gly  Arg  Val  Val  Val  Pro  Gln  Gly  Glu
      85      90      95
Phe  Leu  Thr  Gly  Ala  Ile  His  Leu  Lys  Ser  Asn  Val  Asn  Leu  His  Ile
      100     105     110
Thr  Lys  Gly  Ala  Thr  Val  Lys  Phe  Ser  Thr  Asn  Pro  Lys  Asp  Tyr  Leu
      115     120     125
Pro  Ile  Val  His  Thr  Arg  Trp  Glu  Gly  Met  Glu  Leu  Met  His  Ile  Ser
130     135     140
Pro  Leu  Ile  Tyr  Ala  Tyr  Glu  Gln  Thr  Asn  Ile  Ala  Val  Thr  Gly  Glu
145     150     155     160
Gly  Thr  Leu  Asp  Gly  Gln  Gly  Lys  Ala  Phe  Phe  Trp  Lys  Trp  His  Gly
      165     170     175
Asn  Pro  Arg  Tyr  Gly  Gly  Asn  Pro  Asp  Val  Ile  Ser  Gln  Arg  Pro  Ala
      180     185     190
Arg  Ala  Arg  Leu  Tyr  Glu  Met  Met  Glu  Lys  Gly  Val  Pro  Val  Ala  Glu
      195     200     205
Arg  Ile  Phe  Gly  Glu  Thr  Gln  Tyr  Leu  Arg  Pro  Gln  Phe  Ile  Gln  Pro
210     215     220
Tyr  Lys  Cys  Lys  Asn  Val  Leu  Ile  Glu  Gly  Val  Lys  Ile  Ile  Asp  Ser
225     230     235     240
Pro  Met  Trp  Glu  Val  His  Pro  Val  Leu  Cys  Glu  Asn  Val  Thr  Ile  Arg
      245     250     255
Lys  Leu  His  Ile  Ser  Thr  His  Gly  Pro  Asn  Asn  Asp  Gly  Cys  Asp  Pro
      260     265     270
Glu  Ser  Cys  Lys  Asp  Val  Leu  Ile  Glu  Asp  Cys  Tyr  Phe  Asp  Thr  Gly
      275     280     285
Asp  Asp  Cys  Ile  Ala  Ile  Lys  Ala  Gly  Arg  Asn  Glu  Asp  Gly  Arg  Arg
290     295     300
Ile  Asn  Val  Pro  Thr  Glu  Asn  Val  Val  Val  Arg  Gly  Cys  Val  Met  Lys
305     310     315     320
Asp  Gly  His  Gly  Gly  Ile  Thr  Ile  Gly  Ser  Glu  Ile  Ser  Gly  Gly  Val
      325     330     335
Arg  Asn  Val  Phe  Ala  Glu  Asn  Asn  Arg  Leu  Asp  Ser  Ala  Asp  Leu  Trp
      340     345     350
Thr  Ala  Leu  Arg  Val  Lys  Asn  Asn  Ala  Ser  Arg  Gly  Gly  Lys  Leu  Glu
      355     360     365
Asn  Phe  Tyr  Phe  Arg  Asp  Ile  Thr  Val  Gly  Gln  Val  Ser  Arg  Ala  Val
      370     375     380
Val  Glu  Ile  Asp  Phe  Asn  Tyr  Glu  Glu  Gly  Ala  Lys  Gly  Lys  His  Thr
385     390     395     400
Pro  Val  Val  Arg  Asn  Tyr  Val  Val  Glu  Asn  Leu  Thr  Cys  Asn  Lys  Gly
      405     410     415
Asn  Arg  Ala  Val  Asp  Leu  Gln  Gly  Leu  Asp  Asn  Ala  Pro  Ile  Tyr  Asp

```

			420					425					430		
Ile	Thr	Met	Lys	Asn	Cys	Thr	Phe	Asn	Val	Val	Glu	Lys	Pro	Ser	Val
		435					440					445			
Val	Lys	Asn	Val	Lys	Gly	Val	Lys	Leu	Glu	Asn	Val	Lys	Ile	Asn	Gly
	450					455					460				
Lys	Val	Val	Glu	Ser	Leu	Glu	Asn	Ala	Ala	Thr	Thr	Ala	Lys	Lys	
	465					470					475				

<210>	113
<211>	1017
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

[illegible]

```
<210> 114
<211> 338
<212> PRT
<213> Unknown
```

<220>
<223> Obtained from an environmental sample

```
<221> SIGNAL
<222> (1) ... (18)
```

```
<221> DOMAIN
<222> (19)...(388)
<223> Catalytic domain
```

<400> 114															
Met	Lys	Ile	Phe	Leu	Thr	Ile	Leu	Leu	Ser	Ala	Leu	Phe	Ser	Ile	Ser
1				5					10					15	
Asn	Ala	Gln	Val	Leu	Ser	Asp	Pro	Val	Ala	Asp	Arg	Met	Thr	Ser	Tyr
			20					25					30		
Gln	Leu	Lys	Asn	Gly	Gly	Trp	Pro	Lys	His	Leu	Ala	Asp	Lys	Ser	Val
		35					40					45			
Val	Asn	Tyr	Ser	Lys	Pro	Leu	Ser	Pro	Ala	Leu	Gln	Lys	Val	Ile	Asp
	50					55					60				

Gln Ser Thr Glu Lys Ser Ala Thr Ile Asp Asn Asn Ala Thr Thr Arg
 65 70 75 80
 Glu Ile Asn His Leu Leu Leu Ala Tyr Ser Lys Thr Asn Asn Asp Lys
 85 90 95
 Tyr Leu Gln Ala Ala Thr Lys Gly Val Glu Tyr Ile Leu Ser Ala Gln
 100 105 110
 Asn Asp Lys Gly Gly Trp Pro Gln Tyr Tyr Pro Asp Ser Ser Tyr
 115 120 125
 Arg Gly Gln Ile Thr Tyr Asn Asp Gly Ala Met Ile Asn Val Leu Glu
 130 135 140
 Ile Leu Leu Ser Ile Ser Thr Lys Gln Glu Pro Tyr Ala Val Leu Thr
 145 150 155 160
 Asn Lys Phe Asn Glu Arg Ile Glu Arg Ala Leu Thr Arg Gly Ile His
 165 170 175
 Cys Ile Leu Gln Thr Gln Val Lys Gln Gly Asp Lys Leu Thr Ile Trp
 180 185 190
 Ala Ala Gln Tyr Asp Gln Lys Thr Met Glu Pro Ala Gln Ala Arg Leu
 195 200 205
 Phe Glu Pro Val Ala Leu Ala Thr Ala Glu Ser Ala Gly Ile Leu Arg
 210 215 220
 Phe Leu Met Arg Leu Asp His Pro Thr Pro Glu Ile Lys Asn Ala Ile
 225 230 235 240
 Asn His Ala Val Glu Trp Phe Ser Ser His Lys Glu Val Gly Tyr Asp
 245 250 255
 Tyr Val Lys Thr Glu Lys Asn Gly Lys Leu Leu Arg Asp Leu Val Ser
 260 265 270
 Ser Pro Ala Ser Thr Val Trp Ala Arg Phe Tyr Asp Ile Arg Thr Asn
 275 280 285
 Gln Pro Ile Phe Gly Asp Arg Asp Asn Thr Ile Lys Tyr Ser Leu Asn
 290 295 300
 Glu Ile Ser Glu Glu Arg Gln Asn Gly Tyr Ser Trp Tyr Gly Asn Trp
 305 310 315 320
 Pro Glu Lys Ile Ile Thr Lys Glu Tyr Glu Lys Trp Leu Lys Lys Val
 325 330 335
 Asn Glu

<210> 115
 <211> 996
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 115
 gtggccaagg cgatcggcgg tccgttgccg ccggcaccag ggcagggatc gccggtaacg 60
 tgggcgacga ttctccggca gccatcgccg tggtagcggt ccgcggacgc gaaggcggtt 120
 gccgaaaccg tgcgcgcgag ccagagagcc accggcggct ggccgaagaa cacggattgg 180
 acggcgctcc agagcgacgc tgagcggcag gcgctgcgaa atgcccgcg cgagaccgat 240
 tcgacgatcg acaatggcgc cacggtcacc gagcttcgct ttctcaccgg cgtgtatgtc 300
 gccacgcgcg acgagctttt acgggaggcc gtgcttcgcg gcctcgacta cctgctggcg 360
 tcgcagtaca gcaacggcgg ctggccacaa tactttccgt tgcggaccga ttactcgcgg 420
 gacatcacgt tcaacgacga cgcgatgacc ggctggtgac tgctgctgaa ggatgccgcg 480
 gacgggtcag caggtttcga attcgtcgac aaggcgagac gtgaccgcgc tgccgcggcc 540
 gtgacgcgcg ccacgcgggt gatcctccgc acgcagattc gggtaaacgg tacgctgacc 600
 ggctggtgcc agcagtacga cgccgacgcg ctgacgccgg cgcgcgggcg ctcgtagcag 660
 catccgtcga ttgcgagccg cgagacggtc gggatcgcg ggctgctgat gggcggtgccg 720
 aatccgtcgc cagagatcgt ggctgccgtt gacgcggctg ccgcatggtt gggtaaatcg 780

gaactgaagg	gtgtgcccga	ggcgacggcg	ccaggacttt	gggcgcgctt	ctacgacatc	840
gctacgaatc	ggccgatcta	ttcgggccgc	gacggcgctca	tcaagtaccg	gctcgacgag	900
atcgagctcg	agcggcgcac	aggctacagc	tgggttggcc	cgtacgccgc	ggcattttctg	960
acgaccgaat	atccgaaatg	gcgggcggca	cgatga			996

<210>	116
<211>	331
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

```
<221> DOMAIN
<222> (1)...(331)
<223> Catalytic domain
```

<400>	116														
Met 1	Ala	Lys	Ala	Ile 5	Gly	Gly	Pro	Leu	Pro 10	Pro	Ala	Pro	Gly 15	Gln	Gly
Ser	Pro	Val	Thr 20	Trp	Ala	Thr	Ile	Leu 25	Arg	Gln	Pro	Ser	Pro 30	Trp	Tyr
Ala	Ser	Ala 35	Asp	Ala	Lys	Ala	Val 40	Ala	Glu	Thr	Val	Arg 45	Ala	Ser	Gln
Arg	Ala 50	Thr	Gly	Gly	Trp	Pro 55	Lys	Asn	Thr	Asp	Trp 60	Thr	Ala	Leu	Gln
Ser 65	Asp	Ala	Glu	Arg	Gln 70	Ala	Leu	Arg	Asn	Ala 75	Arg	Ala	Glu	Thr	Asp 80
Ser	Thr	Ile	Asp	Asn 85	Gly	Ala	Thr	Val	Thr 90	Glu	Leu	Arg	Phe	Leu 95	Thr
Arg	Val	Tyr	Val 100	Ala	Thr	Arg	Asp	Glu 105	Leu	Leu	Arg	Glu	Ala 110	Val	Leu
Arg	Gly	Leu	Asp 115	Tyr	Leu	Leu	Ala	Ser	Gln	Tyr	Ser	Asn 125	Gly	Gly	Trp
Pro	Gln 130	Tyr	Phe	Pro	Leu	Arg 135	Thr	Asp	Tyr	Ser	Arg	Asp 140	Ile	Thr	Phe
Asn 145	Asp	Asp	Ala	Met	Thr 150	Gly	Val	Val	Leu	Leu 155	Lys	Asp	Ala	Ala	160
Asp	Gly	Ser	Ala	Gly 165	Phe	Glu	Phe	Val	Asp	Lys 170	Ala	Arg	Arg	Asp 175	Arg
Ala	Ala	Ala	Ala 180	Val	Thr	Arg	Ala	Ile 185	Ala	Val	Ile	Leu	Arg	Thr 190	Gln
Ile	Arg	Val	Asn 195	Gly	Thr	Leu	Thr 200	Gly	Trp	Cys	Gln	Gln 205	Tyr	Asp	Ala
Asp	Ala 210	Leu	Thr	Pro	Ala	Arg 215	Gly	Arg	Ser	Tyr	Glu	His	Pro	Ser	Ile
Ala 225	Ser	Arg	Glu	Thr	Val	Gly 230	Ile	Ala	Arg	Leu	Leu	Met	Gly	Val	Pro
Asn	Pro	Ser	Pro	Glu 245	Ile	Val	Ala	Ala	Val 250	Asp	Ala	Ala	Ala	Ala 255	Trp
Leu	Gly	Lys	Ser 260	Glu	Leu	Lys	Gly	Val 265	Pro	Glu	Ala	Thr	Ala	Pro	Gly
Leu	Trp	Ala	Arg 275	Phe	Tyr	Asp	Ile	Ala	Thr	Asn	Arg	Pro	Ile	Tyr	Ser
Gly	Arg	Asp	Gly 290	Val	Ile	Lys 295	Tyr	Arg	Leu	Asp	Glu	Ile	Glu	Leu	Glu
Arg	Arg	Thr	Gly	Tyr	Ser	Trp	Val	Gly	Pro	Tyr	Ala	Ala	Ala	Phe	Leu
Thr	Thr	Glu	Tyr	Pro	Lys	Trp	Arg	Ala	Ala	Arg					320

325

330

<210> 117
 <211> 1725
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

```

<400> 117
atgaagaatt ttggggtttg taactacaag ttttttgtag cggcaatgtc tgtcgcgtct      60
ttttcgtatg cggcaagcta tacaccccg tcaacagcag tttcgaaaat caacagctat      120
cgaggctatt cggagctgac ttcagctgca tccggcatgg atatcgacca gtacacctac      180
aacatgacca cttggcaaatt cgcaaacggc ggtttttaca aagccatggc cgacaagtat      240
aaaagcgcgt atggcggcgg tcaaaaatcc gaatggcaag ctaaaggcgg tggcgacctc      300
ggcactatag acaacaacgc caccatccag gaaatgcgtt tgctcgccgt gcgttacaaa      360
gaaacgacga acaacaatta caaatccgca ttttaagacaa gtttcaacaa ggcggtcaat      420
tttcttttga ccatgcagcg ctccaaaggc ggactcccac aagtttgcc caaacgcggc      480
aactattctg accaaatcac gctaaatgac aacgccatga tccgcgccat ggtcacgatg      540
atggatatcg ccaacaagac gagtccattt gattcggata tcatcgacga cgccacccgc      600
agcaaaatga aatcggctct cgacaaagcg gtcgattact tgctcaaggc gcaaactcgtg      660
aacgacggaa aggtcacggg atggtgcgcc cagcacgaca ccaacagcct cgccccgta      720
ggcgcacgag cctacgaact cccgagcaaa tccggcaacg aatccatggg cgttgtgtgg      780
tttttgatga actggccaga ccaaaacgaa gcaatccaga aggcggtcaa aggcgcaatc      840
gcttggtaca aaaagaataa actaaaagac aaggcggtta gcaagaccgc aggcgttgtg      900
gacaaggcgg gttcatcgct gtggttccgc ttttacgaag tcaacaacga caactacttt      960
ttctgcgacc gcgatggtgc tagcaccaag acgcaggact tcatgaaaat cagcgaagaa      1020
cgtcgcaagg gctaccagtg ggcaggcgat tacggctctg caattctagg caccgaaaat      1080
gcataccttg aagcactcgc caagatggac gacaactatg ttccacctcc gccagcacca      1140
gctatgtgcg gaaacgacac ttgcaaaacg tacatcgatg gcgttgactt tattgacatt      1200
caaggcggtc aggaacaac caacacggga ttcggttgcg aaggttacgc caacgttgac      1260
aactccaccg gaagctatgt gacctacggc gtcaccgat tcaaggaagg caaatacact      1320
ttgttcatca gctttgcaaa cggcgggtgt tccgcacgcg gttacagcgt ttctgcagga      1380
gacaagacgt tacttgcaag cggcagcatg gaatctacag ccgcatggac cacttggaag      1440
atgcaatcca tcgaaatcga attgccaatg ggctatagcg aactcaagtt cacaagcctt      1500
tcgaaagacg gtatggcgaa catcgattac atcggctgga tgaacgatga tttgaaagtt      1560
ggcgaagttg aagtaccacg ctcatccatt gaagcaatac gcgccatccg caaagcccag      1620
caggacaacc gctactttgt ggactttggc ggcaacaata atagcgcagg ggcttacttt      1680
aagcgtggca tcaacacggt ccgcgtgaat gggaagatga ggtaa      1725

```

<210> 118
 <211> 574
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(24)

<221> DOMAIN
 <222> (25)...(574)
 <223> Catalytic domain

```

<400> 118
Met Lys Asn Phe Gly Phe Gly Asn Tyr Lys Phe Phe Val Ala Ala Met
  1                      5                      10                      15

```

Ser	Val	Ala	Ser	Phe	Ser	Tyr	Ala	Ala	Ser	Tyr	Thr	Pro	Pro	Ser	Thr
			20				25					30			
Ala	Val	Ser	Lys	Ile	Asn	Ser	Tyr	Arg	Gly	Tyr	Ser	Glu	Leu	Thr	Ser
		35					40					45			
Ala	Ala	Ser	Gly	Met	Asp	Ile	Asp	Gln	Tyr	Thr	Tyr	Asn	Met	Thr	Thr
	50				55						60				
Trp	Gln	Ile	Ala	Asn	Gly	Gly	Phe	Tyr	Lys	Ala	Met	Ala	Asp	Lys	Tyr
65				70					75					80	
Lys	Ser	Ala	Tyr	Gly	Gly	Gln	Lys	Ser	Glu	Trp	Gln	Ala	Lys	Gly	
			85				90						95		
Gly	Gly	Asp	Leu	Gly	Thr	Ile	Asp	Asn	Asn	Ala	Thr	Ile	Gln	Glu	Met
		100					105					110			
Arg	Leu	Leu	Ala	Val	Arg	Tyr	Lys	Glu	Thr	Thr	Asn	Asn	Asn	Tyr	Lys
		115					120					125			
Ser	Ala	Phe	Lys	Thr	Ser	Phe	Asn	Lys	Ala	Val	Asn	Phe	Leu	Leu	Thr
	130					135					140				
Met	Gln	Arg	Ser	Lys	Gly	Gly	Leu	Pro	Gln	Val	Trp	Pro	Lys	Arg	Gly
145				150					155					160	
Asn	Tyr	Ser	Asp	Gln	Ile	Thr	Leu	Asn	Asp	Asn	Ala	Met	Ile	Arg	Ala
			165					170					175		
Met	Val	Thr	Met	Met	Asp	Ile	Ala	Asn	Lys	Thr	Ser	Pro	Phe	Asp	Ser
			180					185					190		
Asp	Ile	Ile	Asp	Asp	Ala	Thr	Arg	Ser	Lys	Met	Lys	Ser	Ala	Leu	Asp
	195						200					205			
Lys	Ala	Val	Asp	Tyr	Leu	Leu	Lys	Ala	Gln	Ile	Val	Asn	Asp	Gly	Lys
	210					215					220				
Val	Thr	Val	Trp	Cys	Ala	Gln	His	Asp	Thr	Asn	Ser	Leu	Ala	Pro	Val
225				230					235					240	
Gly	Ala	Arg	Ala	Tyr	Glu	Leu	Pro	Ser	Lys	Ser	Gly	Asn	Glu	Ser	Met
			245					250						255	
Gly	Val	Val	Trp	Phe	Leu	Met	Asn	Trp	Pro	Asp	Gln	Asn	Glu	Ala	Ile
		260						265					270		
Gln	Lys	Ala	Val	Lys	Gly	Ala	Ile	Ala	Trp	Tyr	Lys	Lys	Asn	Lys	Leu
		275					280					285			
Lys	Asp	Lys	Ala	Phe	Ser	Lys	Thr	Ala	Gly	Val	Val	Asp	Lys	Ala	Gly
	290					295					300				
Ser	Ser	Leu	Trp	Phe	Arg	Phe	Tyr	Glu	Val	Asn	Asn	Asp	Asn	Tyr	Phe
305				310					315					320	
Phe	Cys	Asp	Arg	Asp	Gly	Ala	Ser	Thr	Lys	Thr	Gln	Asp	Phe	Met	Lys
			325						330					335	
Ile	Ser	Glu	Glu	Arg	Arg	Lys	Gly	Tyr	Gln	Trp	Ala	Gly	Asp	Tyr	Gly
		340						345					350		
Ser	Ala	Ile	Leu	Gly	Thr	Glu	Asn	Ala	Tyr	Leu	Glu	Ala	Leu	Ala	Lys
		355					360					365			
Met	Asp	Asp													

				485					490					495			
Phe	Thr	Ser	Leu	Ser	Lys	Asp	Gly	Met	Ala	Asn	Ile	Asp	Tyr	Ile	Gly		
			500					505					510				
Trp	Met	Asn	Asp	Asp	Leu	Lys	Val	Gly	Glu	Val	Glu	Val	Pro	Arg	Ser		
		515					520					525					
Ser	Ile	Glu	Ala	Ile	Arg	Ala	Ile	Arg	Lys	Ala	Gln	Gln	Asp	Asn	Arg		
	530					535					540						
Tyr	Phe	Val	Asp	Phe	Gly	Gly	Asn	Asn	Asn	Ser	Ala	Gly	Ala	Tyr	Phe		
545					550					555					560		
Lys	Arg	Gly	Ile	Asn	Thr	Phe	Arg	Val	Asn	Gly	Lys	Met	Arg				
				565					570								

<210> 119
 <211> 1848
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 119

gtgtcatggc	aggaatccgg	tgcggctatc	accaacgcct	ggaatgcaac	gctcagtggc	60
tcaaaccctt	acacagccgt	atccgctggt	tggaatggca	cacttgcccc	caatgcatcg	120
gccacttttg	gtttccaggc	aaacggttct	gccgggtgcac	ctaaagtga	tggcagcttg	180
tgcggcacca	acacttcata	aacaccggca	tccagcagtg	ttgccagctc	ggttaaatca	240
agcgcgccc	tatcgtccag	cagcagatca	tccagttcaa	tcgtatcac	tagcagctct	300
ttagcgagaa	gttctattgc	ctccagcagc	tcactagtta	gtagctccag	agcgagcagt	360
agtgcgcaa	gcgttttctc	ttttacgata	caggaagagc	aagcgggctt	ctgtcgtgtt	420
gatggcattg	cgacagaaa	caccaacacc	ggttttaccg	gcaatggcta	caccaatgcg	480
aacaacgcgc	aaggcgagc	gattgaatgg	gcagtcagcg	cacctagcag	tggccgttat	540
acagtagcct	tccgcttcgc	caatggcggc	acagcagcgc	gcaacggctc	gttggttaac	600
aatggcggtg	gcaatggtaa	ttactactgt	gagttaccoc	tgaccggcgc	atgggcaacc	660
tggcaaattg	ccagcgtgga	aattgattta	gtgcaaggca	ataatatttt	aaaactctcg	720
gcgttaaccg	ctgacggttt	ggccaatata	gactcattaa	aaatagacgg	cgcgcaaacc	780
aaagcaggta	cttgacgac	tacatcaagc	agcagcgttg	ccagcagctc	gtcgtccgtt	840
aaatccagcg	caagttcttc	ttcgagttca	tccaccgctg	caaaaatact	gacattagac	900
ggtaaccggg	ccgccagctg	gttcaacaaa	tccaggacca	agtgggaatag	cagccgcgcc	960
gatatttgtg	tgtcttacca	gcaatccaac	ggcgggttgg	caaaaaacct	ggattacaac	1020
tcagtgaagc	caggcaatgg	cgggagcgac	agcggcacca	tcgacaatgg	tgcaaccatt	1080
accgaaatgg	tttacctcgc	tgaaatttat	aaaaacggcg	gcaacaccaa	atatcgcgat	1140
gcagtgcgca	gagcagcaaa	cttttttagtg	agctcgcaat	acagcacagg	cgccttgcca	1200
caattttatc	cgttgaaagg	cggctatgcg	gatcatgcga	cctttaacga	taacggcatg	1260
gcgtacgcgt	tgacggtatt	ggatttcgca	gtaaacaac	gcgcaccgtt	tgataacgac	1320
attttctctg	attctgatcg	ggcgaaattc	aaaaccgctg	ttgccaaagg	tgtggattac	1380
attttaaaag	cgcagtggaa	acaaaatgga	aaactcactg	catggtgtgc	acaacacggg	1440
gctacggatt	accaaccgaa	aaaagcgcg	gcttatgaat	tggaatcatt	gagtggtagc	1500
gagtcggctg	gcattctcgc	cttcttgatg	acccaaccac	aaaccgcgca	aatcgaagcg	1560
gcgggtcaagg	cgggtgtcaa	ctggttcgcc	agtccaaata	cttatttggc	taactacact	1620
tacgattcat	caaaagcgtc	taccaaccgc	atttgtgata	aatccggaag	cagaatgtgg	1680
tatcgcttct	atgacctgaa	caccaaccgt	ggtttcttta	gtgatcgcca	tggcagcaaa	1740
ttctatgata	tcacccaaat	gtcagaagag	cgtcgcaccg	gttatagctg	gggtggctct	1800
tacggtgaat	ctattatttc	cttcgcgcaa	aaagtgggtt	atctgtaa		1848

<210> 120
 <211> 615
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> BINDING

 $\langle 222 \rangle \quad (1) \dots (61)$

<223> Carbohydrate binding module

<221> BINDING

 $\langle 222 \rangle \quad (134) \dots (257)$

<223> Carbohydrate binding module

<221> DOMAIN

<222> (258) ... (615)

<223> Catalytic domain

$\langle 400 \rangle$ 120

Met	Ser	Trp	Gln	Glu	Ser	Gly	Ala	Ala	Ile	Thr	Asn	Ala	Trp	Asn	Ala
1				5					10					15	
Thr	Leu	Ser	Gly	Ser	Asn	Pro	Tyr	Thr	Ala	Val	Ser	Ala	Gly	Trp	Asn
			20					25					30		
Gly	Thr	Leu	Ala	Pro	Asn	Ala	Ser	Ala	Thr	Phe	Gly	Phe	Gln	Ala	Asn
		35					40				45				
Gly	Ser	Ala	Gly	Ala	Pro	Lys	Val	Asn	Gly	Ser	Leu	Cys	Gly	Thr	Asn
	50					55					60				
Thr	Ser	Ser	Thr	Pro	Ala	Ser	Ser	Ser	Val	Ala	Ser	Ser	Val	Lys	Ser
65				70					75					80	
Ser	Ala	Pro	Val	Ser	Ser	Ser	Ser	Arg	Ser	Ser	Ser	Ser	Ile	Ala	Ile
				85				90					95		
Thr	Ser	Ser	Ser	Leu	Ala	Arg	Ser	Ser	Ile	Ala	Ser	Ser	Ser	Ser	Leu
			100					105					110		
Val	Ser	Ser	Ser	Arg	Ala	Ser	Ser	Ser	Ala	Pro	Ser	Val	Phe	Ser	Phe
		115					120					125			
Thr	Ile	Gln	Glu	Glu	Gln	Ala	Gly	Phe	Cys	Arg	Val	Asp	Gly	Ile	Ala
	130					135					140				
Thr	Glu	Ser	Thr	Asn	Thr	Gly	Phe	Thr	Gly	Asn	Gly	Tyr	Thr	Asn	Ala
145				150					155					160	
Asn	Asn	Ala	Gln	Gly	Ala	Ala	Ile	Glu	Trp	Ala	Val	Ser	Ala	Pro	Ser
				165				170						175	
Ser	Gly	Arg	Tyr	Thr	Val	Ala	Phe	Arg	Phe	Ala	Asn	Gly	Gly	Thr	Ala
			180					185					190		
Ala	Arg	Asn	Gly	Ser	Leu	Leu	Ile	Asn	Gly	Gly	Ser	Asn	Gly	Asn	Tyr
		195					200					205			
Thr	Val	Glu	Leu	Pro	Leu	Thr	Gly	Ala	Trp	Ala	Thr	Trp	Gln	Ile	Ala
	210					215					220				
Ser	Val	Glu	Ile	Asp	Leu	Val	Gln	Gly	Asn	Asn	Ile	Leu	Lys	Leu	Ser
225				230					235					240	
Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Ser	Leu	Lys	Ile	Asp
				245				250						255	
Gly	Ala	Gln	Thr	Lys	Ala	Gly	Thr	Cys	Ser	Thr	Thr	Ser	Ser	Ser	Ser
		260						265					270		
Val	Ala	Ser	Ser	Ser	Ser	Ser	Val	Lys	Ser	Ser	Ala	Ser	Ser	Ser	Ser
		275					280					285			
Ser	Ser	Ser	Thr	Ala	Ala	Lys	Ile	Leu	Thr	Leu	Asp	Gly	Asn	Pro	Ala
	290					295					300				
Ala	Ser	Trp	Phe	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Asn	Ser	Ser	Arg	Ala
305				310					315					320	
Asp	Ile	Val	Leu	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys	Asn
				325					330					335	
Leu	Asp	Tyr	Asn	Ser	Val</										

Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu
 355 360 365
 Ile Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg
 370 375 380
 Ala Ala Asn Phe Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro
 385 390 395 400
 Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn
 405 410 415
 Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn
 420 425 430
 Lys Arg Ala Pro Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala
 435 440 445
 Lys Phe Lys Thr Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala
 450 455 460
 Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly
 465 470 475 480
 Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser
 485 490 495
 Leu Ser Gly Ser Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln
 500 505 510
 Pro Gln Thr Ala Gln Ile Glu Ala Val Lys Ala Gly Val Asn Trp
 515 520 525
 Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser
 530 535 540
 Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met Trp
 545 550 555 560
 Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg
 565 570 575
 Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg
 580 585 590
 Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser Phe
 595 600 605
 Ala Gln Lys Val Gly Tyr Leu
 610 615

<210> 121
 <211> 1047
 <212> DNA
 <213> Bacteria

<400> 121
 atgatgagat caagcatcgt caagctagtt gctttcagtg ttgtgggttat gttatggctc 60
 ggtgtatcct ttcaaacggc agaagcgaat acgccaaatt tcaacttaca aggctttgcc 120
 acgttaaagt ggggaacaac tgggtggtgca ggtggagatg tagtgacggt tcgtacaggg 180
 aatgaattaa taaacgcttt gaagtcctaa aaccctaata gtcggttaac aatttatgta 240
 aacggtacga taacacctag taatacgtct gatagtaaga tcgatattaa ggatgtttcc 300
 aatgtatcga ttttaggggt tggtaacaaat ggacgattaa atgggatcgg tattaagta 360
 tggcgagcga ataatatcat cattcgcaac ttgacgatcc atgaagtcca tacaggtgat 420
 aaagatgcga ttagcattga agggccctct cggaacattt ggattgacca taacgagctt 480
 tatgccagct tgaacgttca taaagaccac tatgacggct tgtttgacgt aaagcgcgat 540
 gcttacaata ttaccttctc ttggaattat gtccatgatg gctggaaagc gatgctcatg 600
 gggaactctg atagtataa ctacgaccga aacataacat tccaccataa ctacttcaaa 660
 aacttaaaact ctgcggtacc tgcgtaccgt tttggaaagg cgcaattgtt tagcaattac 720
 tttgagaaca ttttagaaac aggcattaat tcacggatgg gagcggaat gctcgttgaa 780
 cataacgttt ttgagaatgc caccaaccgg ttaggattct ggcatagcag tcgaacaggt 840
 tattggaatg ttgccaataa ccgctatatc aatagcacgg gtagcatgcc gaccacttcc 900
 acgaccaatt atcgacctcc ttatccctat acggtcacac cagttggtga tgtgaaatcg 960
 gttgtcacac gttatgcggg agttggtgtc atccagccgt atgcaagaaa gccatccgag 1020
 cgattgctct ggtggctttt tgcataa 1047

<210> 122
 <211> 348
 <212> PRT
 <213> Bacteria

<220>

<221> SIGNAL
 <222> (1)...(29)

<221> DOMAIN
 <222> (30)...(348)
 <223> Catalytic domain

<400> 122
 Met Met Arg Ser Ser Ile Val Lys Leu Val Ala Phe Ser Val Val Val
 1 5 10 15
 Met Leu Trp Leu Gly Val Ser Phe Gln Thr Ala Glu Ala Asn Thr Pro
 20 25 30
 Asn Phe Asn Leu Gln Gly Phe Ala Thr Leu Asn Gly Gly Thr Thr Gly
 35 40 45
 Gly Ala Gly Gly Asp Val Val Thr Val Arg Thr Gly Asn Glu Leu Ile
 50 55 60
 Asn Ala Leu Lys Ser Lys Asn Pro Asn Arg Pro Leu Thr Ile Tyr Val
 65 70 75 80
 Asn Gly Thr Ile Thr Pro Ser Asn Thr Ser Asp Ser Lys Ile Asp Ile
 85 90 95
 Lys Asp Val Ser Asn Val Ser Ile Leu Gly Val Gly Thr Asn Gly Arg
 100 105 110
 Leu Asn Gly Ile Gly Ile Lys Val Trp Arg Ala Asn Asn Ile Ile Ile
 115 120 125
 Arg Asn Leu Thr Ile His Glu Val His Thr Gly Asp Lys Asp Ala Ile
 130 135 140
 Ser Ile Glu Gly Pro Ser Arg Asn Ile Trp Ile Asp His Asn Glu Leu
 145 150 155 160
 Tyr Ala Ser Leu Asn Val His Lys Asp His Tyr Asp Gly Leu Phe Asp
 165 170 175
 Val Lys Arg Asp Ala Tyr Asn Ile Thr Phe Ser Trp Asn Tyr Val His
 180 185 190
 Asp Gly Trp Lys Ala Met Leu Met Gly Asn Ser Asp Ser Asp Asn Tyr
 195 200 205
 Asp Arg Asn Ile Thr Phe His His Asn Tyr Phe Lys Asn Leu Asn Ser
 210 215 220
 Arg Val Pro Ala Tyr Arg Phe Gly Lys Ala His Leu Phe Ser Asn Tyr
 225 230 235 240
 Phe Glu Asn Ile Leu Glu Thr Gly Ile Asn Ser Arg Met Gly Ala Glu
 245 250 255
 Met Leu Val Glu His Asn Val Phe Glu Asn Ala Thr Asn Pro Leu Gly
 260 265 270
 Phe Trp His Ser Ser Arg Thr Gly Tyr Trp Asn Val Ala Asn Asn Arg
 275 280 285
 Tyr Ile Asn Ser Thr Gly Ser Met Pro Thr Thr Ser Thr Thr Asn Tyr
 290 295 300
 Arg Pro Pro Tyr Pro Tyr Thr Val Thr Pro Val Gly Asp Val Lys Ser
 305 310 315 320
 Val Val Thr Arg Tyr Ala Gly Val Gly Val Ile Gln Pro Tyr Ala Arg
 325 330 335
 Lys Pro Ser Glu Arg Leu Leu Trp Trp Leu Phe Ala

340

345

<210> 123
 <211> 1830
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 123
 ttgagtctac ttagtgtaat gacccttttg cctgtaatgg caagtaacaa cgtagctccc 60
 tggggctggg ccacctgctc cgatgagtc ggcacagctt atactctgaa cggaggttgc 120
 ttttctgatg catcttccgt tactctgaaa gctcttggca atgaacaaac agatgacaaa 180
 caaatcaaac aggctatcgc tcagaaagac atcattatct tagatgggtc caatggcgat 240
 ttcatcctta atgaatacat caagatttcg accaaaaaca aaaccatcat tggatatcaac 300
 aacgcccgcc tgtgtacaaa gttctaccta accgctgatg atattacgta ccttaaagca 360
 caaggactgg agggactgag tagtacaaat caacatacag gaactctgcc tgatggcaca 420
 acagtgaacct gtgacgagcg tgcctttttc accaagaaag ccatcatgga actccaatat 480
 cagaaaacag gatcctatac cctacccaat aaatcaggtat tcttttattt agatgccgct 540
 tctgagaata tcatcatccg aaatatctcg ctgatagggc caggagccgt agatatagac 600
 ggagctgacc tgattaccaa tcagggttaag cacgtctgga ttgaccattg cacgtttgtg 660
 gactctcaag atggtgccc ggacagcaag gtatgcgact gggccaccta tacctataac 720
 cacttctact atacagaccg cagttactca catgcctaca cttgcggttg cggatgggtc 780
 agcaatcatg aaatggtgat tcacatgacc tttgcatgta atatctgggg agcaaaatgt 840
 atgcgtcgtc tgccgcaagc agatgactgt ttcatacacc ttgtgaacaa ctatcacaa 900
 tgtcctggca atagtgtcgg tatgaccatt aacagttaca gcaaagcatt ggttgagggt 960
 aactatgctg ctgcaggtgt caacaagcca ttagatggca gtggggccaa ccgtaatgta 1020
 acagctaagg ataatagttt tgcaaaactca caagccggtt ctggtgtgtc tgtgccatac 1080
 gactatacca agattgcagc cgccgacgtt ccagctacgc tgactggaac agagggtgca 1140
 ggcgccacat taggcaacga tgcaacatac attctgtcta ctattccaac tgtcgaccga 1200
 caagaaggcg aatcttcaact ctactatttc attgatggcc tgggtgggaac taatagtga 1260
 ggctattcca ttatagagtt taatgatggc gcaacattgc tgctgaacaa taaagagaaa 1320
 gcatggtcta atggtagtgc aattcaactt ggtgacgata attatacgag tattaactt 1380
 tctaattggag cagaaaacat cttcacagca cctactggca aaaaagtaag tggattacc 1440
 ttctattctt atatcaatat aaaagaagaa aaactcgact tcaccaaata tccagaatat 1500
 ggtttccgca cctgtttctg gcagaaagtt gccaacctca cttattctgc gacttctgat 1560
 gacgtacaaa tcttgaaatc tcgtgatcca cagaatactg acgtggcatc attccatttc 1620
 actccaacaa atgttgtaag tttcaaaaat tcaggtgaac agctttgttt cttaatgaaa 1680
 gtcacctata gtgatgaaag cacaggtatc tctgctatcc agaaaaaat gcctatcgat 1740
 ggcgttacct ataaccttca aggtatccgt atagataatc ccaccaaggg aatctatatt 1800
 cagaacggaa agaaaatcat tatcaataa 1830

<210> 124
 <211> 609
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(390)
 <223> Catalytic domain

<400> 124

Leu	Ser	Leu	Leu	Ser	Val	Met	Thr	Leu	Leu	Pro	Val	Met	Ala	Ser	Asn
1				5				10						15	
Asn	Val	Ala	Pro	Trp	Gly	Trp	Ala	Thr	Cys	Ser	Asp	Glu	Ser	Ala	Thr
		20					25						30		
Ala	Tyr	Thr	Leu	Asn	Gly	Gly	Cys	Phe	Ser	Asp	Ala	Ser	Ser	Val	Thr
	35					40					45				
Leu	Lys	Ala	Leu	Gly	Asn	Glu	Gln	Thr	Asp	Asp	Lys	Gln	Ile	Lys	Gln
50					55						60				
Ala	Ile	Ala	Gln	Lys	Asp	Ile	Ile	Ile	Leu	Asp	Gly	Ser	Asn	Gly	Asp
65				70					75					80	
Phe	Ile	Leu	Asn	Glu	Tyr	Ile	Lys	Ile	Ser	Thr	Lys	Asn	Lys	Thr	Ile
			85						90					95	
Ile	Gly	Ile	Asn	Asn	Ala	Arg	Leu	Cys	Thr	Lys	Phe	Tyr	Leu	Thr	Ala
			100					105					110		
Asp	Asp	Ile	Thr	Tyr	Leu	Lys	Ala	Gln	Gly	Leu	Glu	Gly	Leu	Ser	Ser
		115				120						125			
Thr	Asn	Gln	His	Thr	Gly	Thr	Leu	Pro	Asp	Gly	Thr	Thr	Val	Thr	Cys
	130				135						140				
Asp	Glu	Arg	Ala	Phe	Phe	Thr	Lys	Lys	Ala	Ile	Met	Glu	Leu	Gln	Tyr
145				150					155					160	
Gln	Lys	Thr	Gly	Ser	Tyr	Thr	Leu	Pro	Asn	Lys	Ser	Gly	Ile	Phe	Tyr
			165						170					175	
Leu	Asp	Ala	Ala	Ser	Glu	Asn	Ile	Ile	Ile	Arg	Asn	Ile	Ser	Leu	Ile
		180						185					190		
Gly	Pro	Gly	Ala	Val	Asp	Ile	Asp	Gly	Ala	Asp	Leu	Ile	Thr	Asn	Gln
	195					200						205			
Gly	Lys	His	Val	Trp	Ile	Asp	His	Cys	Thr	Phe	Val	Asp	Ser	Gln	Asp
	210				215					220					
Gly	Ala	Leu	Asp	Ser	Lys	Val	Cys	Asp	Trp	Ala	Thr	Tyr	Thr	Tyr	Asn
225				230					235					240	
His	Phe	Tyr	Tyr	Thr	Asp	Arg	Ser	Tyr	Ser	His	Ala	Tyr	Thr	Cys	Gly
			245					250						255	
Cys	Gly	Trp	Val	Ser	Asn	His	Glu	Met	Val	Ile	His	Met	Thr	Phe	Ala
	260						265						270		
Cys	Asn	Ile	Trp	Gly	Ala	Lys	Cys	Met	Arg	Arg	Leu	Pro	Gln	Ala	Asp
	275					280						285			
Asp	Cys	Phe	Ile	His	Leu	Val	Asn	Asn	Tyr	His	Asn	Cys	Pro	Gly	Asn
	290				295						300				
Ser	Val	Gly	Met	Thr	Ile	Asn	Ser	Tyr	Ser	Lys	Ala	Leu	Val	Glu	Gly
305				310					315					320	
Asn	Tyr	Ala	Ala	Ala	Gly	Val	Asn	Lys	Pro	Leu	Asp	Gly	Ser	Gly	Ala
			325					330						335	
Asn	Arg	Asn	Val	Thr	Ala	Lys	Asp	Asn	Ser	Phe	Ala	Asn	Ser	Gln	Ala
		340					345						350		
Gly	Ser	Val	Val	Ser	Val	Pro	Tyr	Asp	Tyr	Thr	Lys	Ile	Ala	Ala	Ala
	355					360						365			
Asp	Val	Pro	Ala	Thr	Leu	Thr	Gly	Thr	Glu	Gly	Ala	Gly	Ala	Thr	Leu
	370				375						380				
Gly	Asn	Asp	Ala	Thr	Tyr	Ile	Leu	Ser	Thr	Ile	Pro	Thr	Val	Asp	Arg
385				390					395					400	
Gln	Glu	Gly	Glu	Ser	Ser	Leu	Tyr	Tyr	Phe	Ile	Asp	Gly	Leu	Val	Gly
			405						410					415	
Thr	Asn	Ser	Glu	Gly	Tyr	Ser	Ile	Ile	Glu	Phe	Asn	Asp	Gly	Ala	Thr
		420					425						430		
Leu	Leu	Leu	Asn	Asn	Lys	Glu	Lys	Ala	Trp	Ser	Asn	Gly	Ser	Ala	Ile
	435					440						445			
Gln	Leu	Gly	Asp	Asp	Asn	Tyr	Thr	Ser	Ile	Lys	Leu	Ser	Asn	Gly	Ala
	450				455						460				
Glu	Asn	Ile	Phe	Thr	Ala	Pro	Thr	Gly	Lys	Lys	Val	Ser	Gly	Ile	Thr

[illegible]

<210>	125
<211>	1170
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample.

<400>	125								
atgagggtcta	aaatcatcag	cgccataaat	aattatagtg	ttattattct	cgatggctcg				60
aatggcgatt	tcactattag	tgctacaatg	agtttcagta	gcaaatcaaa	caaaaccata				120
gttgggtgtaa	ataatgctcg	cctatgcacc	aagtctctatc	taaccgatga	aataaagact				180
gcgctcgatg	ctgctaattg	aaaatcagca	agttcaacca	gtggagggtgg	tacactctca				240
aatgggaaat	cagtgctcaga	acaacgtgaa	taccttactc	gtgaaacaat	tatcgatcta				300
actggcgatg	cttcggaatc	gtgtcagaaa	gcgggcatct	ttagcttcag	tagttgtacc				360
aatatcatca	tgcgaaacct	cgttttggtt	ggccctggcc	catgcgatgt	aggtggcaac				420
gattttgcttt	cgctcactgg	ttctaagcat	ttttgggtcg	atcactgtga	gttaaccgat				480
ggtatagatg	gcaatttcga	tattaccaag	agtagcgatt	tcaatactgt	tacttggtgt				540
atattcaatt	ataccgatcg	tgcatacgac	cacatgaact	ccaatcttat	tggtagctcc				600
gatagcgaag	atgctgccta	tttgaacact	actatggcat	gcaatatttg	gggctacaag				660
tgcaatcagc	gaatgccaat	ggctcggtct	ggtaatatct	acctgtgaa	caacttttac				720
gattgcgctg	gcaatagtgt	ggctgttaac	cctcgtaaaa	attctgagtt	cttagtcgag				780
aactgctact	ttgccacggg	tgtgaagcca	ttctcgcaga	gtgggtgcgtt	gggatacaac				840
tttattgatt	gctatacaga	agattcatac	acttttcagc	agagtggtag	agtgtctgtg				900
ccatacgttt	actctaagtt	tgatgtgcaa	ttagtaccgg	agcaactcaa	taaatatgct				960
ggcgcaacgc	ttactttctcc	gcttgtcata	ggtcgggaag	agggtgttgt	tactcctatt				1020
agtgctgtct	ctggttgatg	cgatgtttgt	ttggtcgaat	actattcgct	gactggtaat				1080
cgtgttaaca	cgctcaatag	aggcataat	atcgttagaa	ctatttacgc	caacggcaaa				1140
gtaaccaacac	aaaagggtttt	ggtgaaatag							1170

<210>	126
<211>	389
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample.

<221> DOMAIN

<222> (24)...(325)

<223> Catalytic domain

<400> 126

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Met Arg Ser Lys Ile Ile Ser Ala Ile Asn Asn Tyr Ser Val Ile Ile
 1           5           10
Leu Asp Gly Ser Asn Gly Asp Phe Thr Ile Ser Ala Thr Met Ser Phe
          20           25           30
Ser Ser Lys Ser Asn Lys Thr Ile Val Gly Val Asn Asn Ala Arg Leu
          35           40           45
Cys Thr Lys Phe Tyr Leu Thr Asp Glu Ile Lys Thr Ala Leu Asp Ala
          50           55           60
Ala Asn Val Lys Ser Ala Ser Ser Thr Ser Gly Gly Gly Thr Leu Ser
65          70          75          80
Asn Gly Lys Ser Val Ser Glu Gln Arg Glu Tyr Leu Thr Arg Gln Thr
          85          90          95
Ile Ile Asp Leu Thr Gly Asp Ala Ser Glu Ser Cys Gln Lys Ala Gly
          100          105          110
Ile Phe Ser Phe Ser Ser Cys Thr Asn Ile Ile Met Arg Asn Leu Val
          115          120          125
Leu Val Gly Pro Gly Pro Cys Asp Val Gly Gly Asn Asp Leu Leu Ser
          130          135          140
Leu Thr Gly Ser Lys His Phe Trp Val Asp His Cys Glu Leu Thr Asp
145          150          155          160
Gly Ile Asp Gly Asn Phe Asp Ile Thr Lys Ser Ser Asp Phe Asn Thr
          165          170          175
Val Thr Trp Cys Ile Phe Asn Tyr Thr Asp Arg Ala Tyr Asp His Met
          180          185          190
Asn Ser Asn Leu Ile Gly Ser Ser Asp Ser Glu Asp Ala Tyr Leu
          195          200          205
Asn Thr Thr Met Ala Cys Asn Ile Trp Gly Tyr Lys Cys Asn Gln Arg
          210          215          220
Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Phe Tyr
225          230          235          240
Asp Cys Ala Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser Glu
          245          250          255
Phe Leu Val Glu Asn Cys Tyr Phe Ala Thr Gly Val Lys Pro Phe Ser
          260          265          270
Gln Ser Gly Ala Leu Gly Tyr Asn Phe Ile Asp Cys Tyr Thr Glu Asp
          275          280          285
Ser Tyr Thr Phe Gln Gln Ser Gly Thr Val Ser Val Pro Tyr Val Tyr
          290          295          300
Ser Lys Phe Asp Val Gln Leu Val Pro Glu Gln Leu Asn Lys Tyr Ala
305          310          315          320
Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Glu Gly Val
          325          330          335
Val Thr Pro Ile Ser Ala Val Ser Val Asp Ser Asp Val Val Leu Val
          340          345          350
Glu Tyr Tyr Ser Leu Thr Gly Asn Arg Val Asn Thr Leu Asn Arg Gly
          355          360          365
Ile Asn Ile Val Arg Thr Ile Tyr Ala Asn Gly Lys Val Thr Thr Gln
          370          375          380
Lys Val Leu Val Lys
385

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<210> 127

<211> 1449

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 127

atgcaatatg	gcaaattagt	acgcttgctg	gcactgacaa	cagcgctggc	attcagcgcc	60
ctggcacagg	caaataacct	ggcaattaca	ggccccggag	ccggggctga	tggttccagc	120
aaagccagtg	gcagtagcta	cggcgatgta	aaagacgccg	atctgcaaag	ctactggcaa	180
ccgcctgcta	ataacggcca	aagagtgtcg	gttaagtggg	gcagcgctat	cagcggttaat	240
caggtaatat	tgcgtgaaca	gggcagtaat	gtaaccagct	ggcggctggt	aaataatgac	300
aacggcgag	tattggcaac	cggcaccagc	attggcagca	acagaacggt	taacttcagc	360
actgtaagca	cgaaaaaact	caatctggaa	atactaactg	ccagcggtgc	cccgcgcatt	420
gctgagtttg	aagttttattt	aaataccaat	ggcggcaacc	cgccaaatcc	tactgacccg	480
gaaccaggcc	cggtaacttc	ttgcgcagcg	tctccacagg	gctatgcctc	gcttaacggt	540
ggcactaccg	gcggcagtg	cagcaacgcg	gtcacggtaa	cggtaagcac	cggcgctcaa	600
atggtagcgg	cgctacaaaa	ccgcgatcta	aaccggccgc	tcactatccg	ggttaatggc	660
actatcacac	cgggtaattc	tggcgggtgc	agtaagtttg	acattaaaga	tatggataat	720
gtcagcatta	ttggtgtagg	caacaatgcg	ttgtttgacg	gtatcgggtat	taaaatctgg	780
cgggccaata	acgtttattat	ccgcaacctt	acaatgcgtt	atgttaacac	cggcgataaaa	840
gacgctatta	ccattgaagg	cccggcgcg	aatatctgga	ttgaccacaa	cgaaatctat	900
aacagcctga	atgtgggtaa	agattttttac	gacgagctta	taagcggtaa	aaaagacgta	960
gataacgtaa	ctatctctta	caactacctg	cacgacagct	ggaaaacctc	gctgtggggc	1020
agcagtgtat	ccgacaacta	caaccgccgt	attacctttc	accataacca	ctggcataag	1080
gtaaattcac	gcctgccact	gttccgtttt	ggccaggggc	atattttacaa	taactattac	1140
aacgacattc	aggacaccgg	tattaacagc	cggatgggtg	cggtaattcg	tattgaaaac	1200
aatgtgtttg	aaaacgcgaa	aaacccgata	gtgtcgtttt	attccagcgg	ctacggttac	1260
tgggacaccc	gcggtaatag	ctttagcaat	attacctggc	aggaataccc	cagcgacggc	1320
attatcgccg	ggccaaatgt	acaaccacac	gcggtgctaa	acctgcccta	cagctttaac	1380
ctgttaccca	ccaaccaggt	aaaagcccac	gtactggcca	acgccggcgt	gaataaatgt	1440
agttttctaa						1449

<210> 128

<211> 482

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(24)

<221> DOMAIN

<222> (5)...(482)

<223> Catalytic domain

<400> 128

Met	Gln	Tyr	Gly	Lys	Leu	Val	Arg	Leu	Ser	Ala	Leu	Thr	Thr	Ala	Leu
1				5				10						15	
Ala	Phe	Ser	Ala	Leu	Ala	Gln	Ala	Asn	Asn	Leu	Ala	Ile	Thr	Gly	Pro
			20					25					30		
Gly	Ala	Gly	Ala	Asp	Gly	Ser	Ser	Lys	Ala	Ser	Gly	Ser	Ser	Tyr	Gly
			35					40				45			
Asp	Val	Lys	Asp	Ala	Asp	Leu	Gln	Ser	Tyr	Trp	Gln	Pro	Pro	Ala	Asn
			50			55					60				
Asn	Gly	Gln	Arg	Val	Ser	Val	Lys	Trp	Ser	Ser	Ala	Ile	Ser	Val	Asn
65					70				75					80	
Gln	Val	Ile	Leu	Arg	Glu	Gln	Gly	Ser	Asn	Val	Thr	Ser	Trp	Arg	Leu
				85					90					95	

Val	Asn	Asn	Asp	Asn	Gly	Ala	Val	Leu	Ala	Thr	Gly	Thr	Ser	Ile	Gly	100	105	110
Ser	Asn	Arg	Thr	Val	Asn	Phe	Ser	Thr	Val	Ser	Thr	Lys	Lys	Leu	Asn	115	120	125
Leu	Glu	Ile	Leu	Thr	Ala	Ser	Gly	Ala	Pro	Arg	Ile	Ala	Glu	Phe	Glu	130	135	140
Val	Tyr	Leu	Asn	Thr	Asn	Gly	Gly	Asn	Pro	Pro	Asn	Pro	Thr	Asp	Pro	145	150	155
Glu	Pro	Gly	Pro	Val	Thr	Ser	Cys	Ala	Ala	Ser	Pro	Gln	Gly	Tyr	Ala	165	170	175
Ser	Leu	Asn	Gly	Gly	Thr	Thr	Gly	Gly	Ser	Gly	Ser	Asn	Ala	Val	Thr	180	185	190
Val	Thr	Val	Ser	Thr	Gly	Ala	Gln	Met	Val	Ser	Ala	Leu	Gln	Asn	Arg	195	200	205
Asp	Leu	Asn	Arg	Pro	Leu	Thr	Ile	Arg	Val	Asn	Gly	Thr	Ile	Thr	Pro	210	215	220
Gly	Asn	Ser	Gly	Gly	Val	Ser	Lys	Phe	Asp	Ile	Lys	Asp	Met	Asp	Asn	225	230	235
Val	Ser	Ile	Ile	Gly	Val	Gly	Asn	Asn	Ala	Leu	Phe	Asp	Gly	Ile	Gly	245	250	255
Ile	Lys	Ile	Trp	Arg	Ala	Asn	Asn	Val	Ile	Ile	Arg	Asn	Leu	Thr	Met	260	265	270
Arg	Tyr	Val	Asn	Thr	Gly	Asp	Lys	Asp	Ala	Ile	Thr	Ile	Glu	Gly	Pro	275	280	285
Ala	Arg	Asn	Ile	Trp	Ile	Asp	His	Asn	Glu	Ile	Tyr	Asn	Ser	Leu	Asn	290	295	300
Val	Gly	Lys	Asp	Phe	Tyr	Asp	Glu	Leu	Ile	Ser	Gly	Lys	Lys	Asp	Val	305	310	315
Asp	Asn	Val	Thr	Ile	Ser	Tyr	Asn	Tyr	Leu	His	Asp	Ser	Trp	Lys	Thr	325	330	335
Ser	Leu	Trp	Gly	Ser	Ser	Asp	Ser	Asp	Asn	Tyr	Asn	Arg	Arg	Ile	Thr	340	345	350
Phe	His	His	Asn	His	Trp	His	Lys	Val	Asn	Ser	Arg	Leu	Pro	Leu	Phe	355	360	365
Arg	Phe	Gly	Gln	Gly	His	Ile	Tyr	Asn	Asn	Tyr	Tyr	Asn	Asp	Ile	Gln	370	375	380
Asp	Thr	Gly	Ile	Asn	Ser	Arg	Met	Gly	Ala	Val	Ile	Arg	Ile	Glu	Asn	385	390	395
Asn	Val	Phe	Glu	Asn	Ala	Lys	Asn	Pro	Ile	Val	Ser	Phe	Tyr	Ser	Ser	405	410	415
Gly	Tyr	Gly	Tyr	Trp	Asp	Thr	Arg	Gly	Asn	Ser	Phe	Ser	Asn	Ile	Thr	420	425	430
Trp	Gln	Glu	Tyr	Pro	Ser	Asp	Gly	Ile	Ile	Ala	Gly	Pro	Asn	Val	Gln	435	440	445
Pro	Thr	Ala	Val	Leu	Asn	Leu	Pro	Tyr	Ser	Phe	Asn	Leu	Leu	Pro	Thr	450	455	460
Asn	Gln	Val	Lys	Ala	His	Val	Leu	Ala	Asn	Ala	Gly	Val	Asn	Lys	Cys	465	470	475
Ser	Phe																	480

<210> 129

<211> 1173

<212> DNA

<213> Bacillus halodurans ATCC 27557

<220>

<400> 129

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atgagttcga aaatcaaaaa tgctatcaat aactatagtg ttattattct cgatggctcg      60
aatggcgatt ttacagtcaa tgctacaatg agtttcagtg gcaagtccaa taaaactatt      120
gtgggtgtga acaatgctcg cctatgcacc aaattctaca ttacgcccga gataaaagaa      180
gccctcgatg ctgccgatgt gaaatctaag agctcaagta gtggcactgg tggaaactctt      240
tctaattgta cgtcggtcag tgaggctcgc gaattggcta ctcgtcaaac gttgattgat      300
tatctcggcg atagctcaga atcgtatcag aaagctggta tctttggctt tagcaactgc      360
actaatatta ttatgcgcaa cattgttttc gttggccctg gtccatgcga tgtagggtggc      420
aacgacttgc tttcgtctgt tggttcgaag catttctggg tcgaccactg cgagtttacc      480
gatggcatcg atggcaactt cgacatcacc aagagtagcg acttcaacac cgtttcgtgg      540
tgcactttca gctataccga ccgcgcatac gaccacatga attccaacct tattggtagc      600
tccgattcag agaatgcggc ttaccttaat actactatgg cttccaacgt ctggggcaat      660
aagtgcaatc agcgtatgcc tatggctcgt gccggtaata ttcacctcgt aaataattat      720
tacaactgcc ctggcaatag cgtggctgtg aatcctcgca aaaactcaga atttttggtg      780
gagaattgct atttcgcaag tggcgtaaag cctttctcgc agagcggcgc tcttagctat      840
ctatttatcg attgctacac cgaagatact tacaccttcc agaaatctgg ctctactacg      900
gtgccataca catatagcaa attcgaatgc cagcttggtc ccgagcaact caccacaattc      960
gctggcgcaa cattgacttc gccgcttggt attggtaggg aatctgagaa tgttacacca     1020
gtctcagtcg ttgctgcaaa tagcgatgtc atatctgtag aatactattc gctcactggc     1080
aagcgcacat gcgaaccaac taaaggcatc aatatcgtaa gaactattta tactaacggc     1140
aacgtgacca cacaaaaggt cttggtgaaa taa                                     1173

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<210> 130

<211> 390

<212> PRT

<213> Bacillus halodurans ATCC 27557

<220>

<221> DOMAIN

<222> (38)...(326)

<223> Catalytic domain

<400> 130

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Met Ser Ser Lys Ile Lys Asn Ala Ile Asn Asn Tyr Ser Val Ile Ile
  1           5           10           15
Leu Asp Gly Ser Asn Gly Asp Phe Thr Val Asn Ala Thr Met Ser Phe
      20           25           30
Ser Gly Lys Ser Asn Lys Thr Ile Val Gly Val Asn Asn Ala Arg Leu
      35           40           45
Cys Thr Lys Phe Tyr Ile Thr Pro Glu Ile Lys Glu Ala Leu Asp Ala
      50           55           60
Ala Asp Val Lys Ser Lys Ser Ser Ser Ser Gly Thr Gly Gly Thr Leu
      65           70           75           80
Ser Asn Gly Thr Ser Val Ser Glu Ala Arg Glu Leu Ala Thr Arg Gln
      85           90           95
Thr Leu Ile Asp Tyr Leu Gly Asp Ser Ser Glu Ser Tyr Gln Lys Ala
      100          105          110
Gly Ile Phe Gly Phe Ser Asn Cys Thr Asn Ile Ile Met Arg Asn Ile
      115          120          125
Val Phe Val Gly Pro Gly Pro Cys Asp Val Gly Gly Asn Asp Leu Leu
      130          135          140
Ser Leu Val Gly Ser Lys His Phe Trp Val Asp His Cys Glu Phe Thr
      145          150          155          160
Asp Gly Ile Asp Gly Asn Phe Asp Ile Thr Lys Ser Ser Asp Phe Asn
      165          170          175
Thr Val Ser Trp Cys Thr Phe Ser Tyr Thr Asp Arg Ala Tyr Asp His
      180          185          190
Met Asn Ser Asn Leu Ile Gly Ser Ser Asp Ser Glu Asn Ala Ala Tyr
      195          200          205

```

Leu Asn Thr Thr Met Ala Ser Asn Val Trp Gly Asn Lys Cys Asn Gln
 210 215 220
 Arg Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Tyr
 225 230 235 240
 Tyr Asn Cys Pro Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser
 245 250 255
 Glu Phe Leu Val Glu Asn Cys Tyr Phe Ala Ser Gly Val Lys Pro Phe
 260 265 270
 Ser Gln Ser Gly Ala Leu Ser Tyr Leu Phe Ile Asp Cys Tyr Thr Glu
 275 280 285
 Asp Thr Tyr Thr Phe Gln Lys Ser Gly Ser Thr Thr Val Pro Tyr Thr
 290 295 300
 Tyr Ser Lys Phe Asp Ala Gln Leu Val Pro Glu Gln Leu Thr Gln Phe
 305 310 315 320
 Ala Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Ser Glu
 325 330 335
 Asn Val Thr Pro Val Ser Val Ile Ala Ala Asn Ser Asp Val Ile Ser
 340 345 350
 Val Glu Tyr Tyr Ser Leu Thr Gly Lys Arg Ile Ser Glu Pro Thr Lys
 355 360 365
 Gly Ile Asn Ile Val Arg Thr Ile Tyr Thr Asn Gly Asn Val Thr Thr
 370 375 380
 Gln Lys Val Leu Val Lys
 385 390

<210> 131
 <211> 972
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 131
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 accaagtggga atagcagccg cgccgatatt gtgttgtctt accagcaatc caacggcggg 120
 tggcaaaaaa acctggatta caactcagtg agcgcaggca atggcgaggag cgacagcggc 180
 accatcgaca atggtgcaac cattaccgaa atggtttacc tcgctgaaat ttataaaaac 240
 ggcgggcaaca ccaaatatcg cgatgcagtg cgcagagcag caaacttttt agtgagctcg 300
 caatacacgca caggcgccct gccacaattt tatccgttga aaggcgggcta tgcggatcat 360
 gcgaccttta acgataacgg catggcggtac gcgttgacgg tattggattt cgcagtaaac 420
 aaacgcgcac cgtttgataa cgacattttc tctgattctg atcgggcgaa attcaaaacc 480
 gctgttgcca aagggtgtgga ttacatttta aaagcgcagt ggaaacaaaa tggaaaactc 540
 actgcatggt gtgcacaaca cgggtgctacg gattaccaac cgaaaaaagc gcgcgcttat 600
 gaattggaat cattgagtgg tagcgagtcg gtcggcattc tcgccttctt gatgacccaa 660
 ccacaaaccg cgcaaatcga agcggcggtc aaggcgggtg tcaactgggt cgccagtcca 720
 aatacttatt tggctaacta cacttacgat tcatcaaaag cgtctaccaa cccgattgtg 780
 tataaatccg gaagcagaat gtggtatcgc ttctatgacc tgaacaccaa ccgtgggttc 840
 tttagtgatc gcgatggcag caaattctat gatatcacc aaatgtcaga agagcgtcgc 900
 accggttata gctgggggtg ctcttacggt gaatctatta tttccttcgc gcaaaaagtg 960
 gggttatctgt ag 972

<210> 132
 <211> 323
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 132

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Met Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro Ala Ala Ser Trp Phe
 1           5           10           15
Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg Ala Asp Ile Val Leu
 20           25           30
Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn Leu Asp Tyr Asn
 35           40           45
Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly Thr Ile Asp Asn
 50           55           60
Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Ile Tyr Lys Asn
 65           70           75           80
Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe
 85           90           95
Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro
 100          105          110
Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn Asp Asn Gly Met
 115          120          125
Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn Lys Arg Ala Pro
 130          135          140
Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala Lys Phe Lys Thr
 145          150          155          160
Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala Gln Trp Lys Gln
 165          170          175
Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly Ala Thr Asp Tyr
 180          185          190
Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Ser
 195          200          205
Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Ala
 210          215          220
Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp Phe Ala Ser Pro
 225          230          235          240
Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser Lys Ala Ser Thr
 245          250          255
Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met Trp Tyr Arg Phe Tyr
 260          265          270
Asp Leu Asn Thr Asn Arg Gly Phe Ser Asp Arg Asp Gly Ser Lys
 275          280          285
Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser
 290          295          300
Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser Phe Ala Gln Lys Val
 305          310          315          320
Gly Tyr Leu

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<210> 133

<211> 972

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated polynucleotide

<400> 133

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atggcaaaaa tactgacatt agacggtaac ccggccgccca gctggttcaa caaatccagg      60
accaagtgga atagcagccg cgccgatatt gtgtgtgttt accagcaatc caacggcggt      120
tggccaaaaa acctggatta caactcagtg agcgcaggca atggcgggag cgacagcggc      180
accatcgaca atggtgcaac cattaccgaa atggtttacc tcgctgaaat ttataaaaac      240
ggcggcaaca ccaaatatcg cgatgcagtg cgcagagcag caaacttttt agtgagctcg      300

```

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caatacagca caggcgccctt gccacaattt tatccggttga aaggcgggcta tcatgatcat 360
gcgaccttta acgataacgg catggcgtac gcgttgacgg tattggattt cgcagtaaac 420
aaacgcgcac cgtttgataa cgacattttc tctgattctg atcgggcgaa attcaaaacc 480
gctggttgcca aaggtgtgga ttacatttta aaagcgcagt ggaaacaaaa tggaaaactc 540
actgcatggt gtgcacaaca cgggtgctttg gattaccaac cgaaaaaagg tcgcgcttat 600
gaattggaat cattgagtgg taaggagtcg gtcggcattc tcgccttctt gatgacccaa 660
ccacaaaccg cgcaaatacg agcggcggtc aaggcgggtg tcaactgggt cgccagtcca 720
aatacttatt tggctaacta cacttacgat tcatcaaaag cgtctaccaa cccgattgtg 780
tataaaaaagg gaagcagaat gtggtatcgc ttctatgacc tgtataccaa ccgtgggttc 840
tttagtgatc gcgatggcag caaattctat gatatcaccc aaatgtcaga agagcgtcgc 900
accggttata gctgggggtg ctcttggggg gaagttatta tttccttcgc gcaaaaagtg 960
ggttatctgt ag 972

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<210> 134

<211> 323

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated polypeptide

<400> 134

```

Met Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro Ala Ala Ser Trp Phe
 1           5           10           15
Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg Ala Asp Ile Val Leu
      20           25           30
Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn Leu Asp Tyr Asn
      35           40           45
Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly Thr Ile Asp Asn
      50           55           60
Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Ile Tyr Lys Asn
      65           70           75           80
Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe
      85           90           95
Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro
      100          105          110
Leu Lys Gly Tyr His Asp His Ala Thr Phe Asn Asp Asn Gly Met
      115          120          125
Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn Lys Arg Ala Pro
      130          135          140
Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala Lys Phe Lys Thr
      145          150          155          160
Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala Gln Trp Lys Gln
      165          170          175
Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly Ala Leu Asp Tyr
      180          185          190
Gln Pro Lys Lys Gly Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Lys
      195          200          205
Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Ala
      210          215          220
Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp Phe Ala Ser Pro
      225          230          235          240
Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser Lys Ala Ser Thr
      245          250          255
Asn Pro Ile Val Tyr Lys Lys Gly Ser Arg Met Trp Tyr Arg Phe Tyr
      260          265          270
Asp Leu Tyr Thr Asn Arg Gly Phe Phe Ser Asp Arg Asp Gly Ser Lys
      275          280          285
Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser

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	290					295						300					
Trp	Gly	Gly	Ser	Trp	Gly	Glu	Val	Ile	Ile	Ser	Phe	Ala	Gln	Lys	Val		
305					310					315						320	
Gly	Tyr	Leu															